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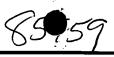
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## STIC-Biotech/ChemLib



From: Sent: To: Subject: Tuesday, February 04, 2003 11:23 AM STIC-Biotech/ChemLib Sequence search of Application NO: 09/775,181

Please do a standard search of SEQ ID NOS: 1, 2, and 4 against both the commercial and interference nucleic acid databases.

Thank you very much!

Ruixiang Li GAU 1646 CM1 8E18 Mail Box 10C01 306-0282

Point of Contact: Toby Port Technical Info. Specialist CM1 6A04 703-308-3534

Searcner:
Phone:
Location:
Date Picked Up: 25
Date Completed: 120
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
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VENDOR/COST (where applic.)
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DEFINITION source ORGANISM ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS TITLE BASE COUNT 3121 3121 3181 3181 3241 3241 3301 3301 3361 3421 3421 3481 3481 3541 3541 3601 3601 Н 3361 61 JOURNAL FEATURES ORIGIN Óγ Pp Pp δ g q g δ a ò g ò g δ qq q Qγ Qγ QY ò ò

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/tissue_type="substantia nigra"
/clone_lib="BRSSN2"
/note="cloning vector: pME18SFL3"
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/clone="BRSSN2000312"
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Sogai, T. and Yamamoto, J.
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Isogal, T. auu temmunour, Isogal, FLJ Project(HRI Team); 2-6-7 Submitted (04-JUL-2002) Takao Isogal, FLJ Project(HRI Team); 2-6-7 Kazuaa-Kamatari, Kisarazu, Chiba 292-0812, Japan Kazuaa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomicséhri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB) inbrary construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Frailmation; clone selection for full insert sequencing: HRI and
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Tanai,H., Watanabe,S., Ishida,S., Ono,Y., Hotuta,T., Watanabe,M.,
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
Yamamoto,J., Isono,Y., Kawai-Hio,Y., Satto,K., Nishikawa,T.,
Kimura,K., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Kanda,K.,
Wagatsuma,M., Takahashi-Fujii,A., Oshima,A., Sugiyama,A.,
Kawakami,B., Suzuki,Y., Sugano,S., Nagahari,K., Masuho,Y., Nagai,K.
MEDO, human cDNA sequencing project
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clone:BRSSN2000312.
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/product="KIAA1136 protein"
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                                                                                                                                                                                                                                                                                                                       SQEEETTENSTLESLSGKKLTQKLKEDSEAESTESVPLVCKSASAHNIJSSEKKTGHPR
TSMLQKSLSVTASAKEKTLGLAGKTQTAGVEERTKSQKPLFNCKETNRHSNSDNTET
KDPAPQUSNEAEEPRFQKSGLIMKQRKVHPTANSDINPGTTQMKDRDIGVEPEV
YDLTPGPVPSESKVQKHVSITAASEMEKNPTFSLKEKSHHKPRAAEVCQQSNQKRIDKA
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KTENENLANGIGHQEKKTSSEENVRGSYNSSNNFQQPLTSRAEVCPWEFETPAQPNAG
RSVALPASAANKIAGSKEEIWDSFKV"
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Ohara,O., Nagase,T. and Kikuno,R.
Direct Submission
Submitted (04-0CT-1999) Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
URL:http://www.kazusa.or.jp/huge/, Tel:+81-438-52-3913,
On May 9, 2002 this sequence version replaced gi:6382013.
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/clone_lib="pBluescriptII SK plus"
/dev_stage="adult"
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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Homo sapiens mRNA for KIAA1136 F
AB032962
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AL Submitted (04-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, Submitted (04-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, Submitted (04-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, Cablo 15A, UK. E-mail enquiries: humquery@sanger.ac.uk on Sep 6, 2001 this sequence version replaced gi:15041820. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotation some. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP thtp://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 constructed by the Sanger 
                                                                                                                                               Human DNA sequence from clone RP11-561H23 on chromosome 10, AL35587
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1larity 99.9%; Pred. No. 0;
Conservative 0; Mismatches 1;
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Assembly program: XGAP4, version 4.5
Sequencing vector: plasmid: L08752; 100% of reads
Chemistry: Dye-terminator Big Dye, 100% of reads
Consensus quality: 147964 bases at least 040
Consensus quality: 149796 bases at least 030
Consensus quality: 150620 bases at least 020
Insert size: 151309; sum-of-contigs
Insert size: 173376; 22.8% error; agarose-fp
Quality coverage: 4.61x in 020 bases; sum-of-contigs Quality
coverage: 4.08x in 020 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                 NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8252 82721: gap of 100 bp 82622 82721: gap of 100 bp 82722 924111: contig of 13611 bp in length 8272 924111: contig of 9690 bp in length 92512 107868: contig of 15357 bp in length 107869 107968: gap of 100 bp 100 bp 129485: contig of 21517 bp in length 107969 129485: contig of 21517 bp in length
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14093 59903: contig of 45811 bp in length
59904 60003: gap of 100 bp
60004 68910: contig of 8907 bp in length
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138674 152209: contig of 13536 bp in length
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4982 13992: contig of 9011 bp in length
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/note="assembly_fragment:01537
fragment_chain:2"
92512. .107868
/note="assembly_fragment:00515
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/note="assembly_fragment:00809
fragment_chain:1"
14093. .59903
/note="assembly_fragment:01674
fragment_chain:2"
/note="assembly_fragment:01032
fragment_chain:2"
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/note="assembly_fragment:02296
fragment_chain:1
                        Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
------ Project Information
                                                                                                             Summary Statistics
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                                                                                       Center project name: bB18101
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Direct Submission
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HTG 19-DEC-2001
SEQUENCING IN
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Direct Submission
Submitted (18-DEC-2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: hunduery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Dec 20, 2001 this sequence version replaced gi:14141526.
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                                                                 ACCCCTGGTCCTGTGCCTTCAGAATCAAAAGTTCAAAAGCACGTATCTATTGTGGCTTCT
                                                                                                                                GAAATGGAGAAAACCCCACTTTTCCTTAAAGGAGAAATCTCACCACAAGCCTAAGGCA
                                                                                                                                               GAAATGGAGAAAAACCCCACTTTTTCCTTAAAGGAGAAATCTCACACAAGCCTAAGGA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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RP13-112H19, ***
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HTG; HTGS_PHASEI; HTGS_FULLTOP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AL591477 168608 bp
Homo sapiens chromosome 10 clone
PROGRESS ***, 3 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                        Insert size: 168408; sum-of-contigs
Insert size: 15446; agarose-fp
Quality coverage: 9.85x in Q20 bases; sum-of-contigs Quality
coverage: 10.88x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGAGACGCATTACGGAGATCCCAGAGACAGTCAGCCGGCAGTGCTCTAAAGAGGACAAG
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                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 168608
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                                                         Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 16754 bases at least Q40
Consensus quality: 167716 bases at least Q30
Consensus quality: 167994 bases at least Q20
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/note="assembly_fragment:00906
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/db_xref="taxon:9606"
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/clone_lib="RPCI-13.1"
Contact: humquery@sanger.ac.uk
                                           Center project name: bB112H19
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1. .168608
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144004 ATTATGAAACAACAAAGGGTCAACCCCACCACTGCCAATTCTGACCTGAACCCAGGCACC
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Rat
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Rattus norvegicus clone CH230-413023, *** SEQUENCING IN PROGRESS
***, 49 unordered pieces.
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                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 49 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                           NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                            Sequencing vector: Jlasmid:
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 101614 bases at least Q40
Consensus quality: 108377 bases at least Q30
Consensus quality: 112616 bases at least Q20
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                                              Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Center: Baylor College of Medicine
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                                                                                                                         Center project name: KAED
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Pred. No. 1.2e-229;
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R. Sitel: Drail (CACCATGTG)

R. Sitel: Drail (CACCATGTG)

Description: 1st strand cDNA was primed with an oligo(dT) primer (ATGTGGCCTTTTTTTTTTTTTTTTTT double-stranded cDNA was synthesized using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with Sfil and size selection was performed to exclude fragments <1.5kb.The Sfil-digested PCR product was cloned into distinct Drail sites of pME18S-FL3. XhoI sites just outside the Drail sites can be used to isolate the cDNA insert. Libraries were constructed by Sugano et al. (University of Tokyo, Institute of Medical Science). Custom primer used for sequencing

(5' end primer [CTTGGTCTGAAAAGCTGCG];
                                                                                                                                                                                                                                                                                                                                                                                                                          PRI 09-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lab host:

(bases 1 to 1857)

Hashimoto, K., Osada, N., Hida, M., Kusuda, J. and Sugano, S.

Direct Submission

Submitted (16-DEC-2000) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan (E-mail:khashi@nih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/, Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)
                                                                                                                                                                                                                                          125572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Euteleostomi;
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                                                                                                                                               3581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AB052146.1 GI:11611572
fis (full insert sequence).
Macaca fascicularis adult male cerebellum cortex cDNA to mRNA,
clone_itb:macaque brain cDNA library QccE clone:QccE-20671.
Macaca fascicularis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Osada,N., Hida,M., Kusuda,J., Tanuma,R., Iseki,K., Hirai,M., Terao,K., Suzuki,Y., Sugano,S. and Hashimoto,K.
Isolation of full-length cDNA clones from macaque brain cDNA
CAACCAAATAGGACACCAGGAAAAAAAACACATCTTCTTGAGGAGAATGTGCGTGGCTC
                  CTATAACTCAAGTAATAACTTCCAGCAACCTTTAACATCACGAGCAGAGGTTTGTCCTTG
                                                                                                                                             GGAGTTTGAGACCCCAGCTCAACCAAATGCTGGAAGAAGTGTAGCTTTACCTGCCTCTTC
                                                                                                                                                                               125571 GGAGTTCGAGCCCCTAGAACAACCAAATGCTGAAAGAATCGTAGCTTTACCCGCCTCCTC
                                                                                                                                                                                                                     TGCTCTAAGTGCAAATAAGATAGCAGGGCCTAGGAAAGAAGAGATCTGGGATAGTTTTAA
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Catarrhini; Cercopithecidae;
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/clone_lib="macaque brain cDNA library QccE"
/dev_stage="adult"
213. 1166
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AB052146
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/db_xref="taxon:9541"
/clone="QccE-20671"
                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA
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Location/Qualifiers
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Mammalia; Eutheria; Primates;
Cercopithecinae; Macaca.
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Unpublished
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| AATGTA 125446
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TITLE
JOURNAL
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LOCUS

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/product="hypothetical protein"
/protein_id="BAB19001.1"
/db_xref="c1:11611573"
/translation="MLQKSLSVIASAKEKTLGLAGKTQTAGVEESAKSQKPLPKDKET
NRNHSNSDNTETKDPPONSNRAEEPRKPQKSGIMKOORVNPTTANSDLNPGATOMKD
NFDIGEVCPWEVYDLTPGPVPSESKVQKHVSIVASEMEKNPTLSLKEKSHHKPKAAEV
                                                                                                                                       CQQSNQKCTDKAEVCLWGIQGQSILEDEKHFISKTPVLQERAKEENGGQPHAAKVCAG
QSEELPPKAVASKTENENLNQIGHQEKKTSFEENVRGSYNSSNNFQQPLMSRAEVCPW
EFETPAQPNAGRSVALPVSSALSASKIAGPRKEEVWDTFKV"
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es 47;
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Pred. No. 2.5e-
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Best Local Similarity 95.7%;
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 209802)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (08-JUL-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Jul 10, 2002 this sequence version replaced g1:21667969.
                                                                                                                                                            3499
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                                                                                                                                                                                                                                                                             1077
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209802 bp DNA linear HTG 09-JUL-Mus musculus chromosome 2 clone RP23-133816, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces.
                                                                                                                     957
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Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 200844 bases at least Q40
Consensus quality: 209515 bases at least Q30
Insert size: 209402; sum-of-contigs
Insert size: 194408; 1.3% error; agarose-fp
Quality coverage: 8.01x in Q20 bases; sum-of-contigs
coverage: 8.63x in Q20 bases; sum-of-contigs
3320 CTCGTGCAGCCAATGTGTGTGTGCTGGGCAGAGCGAAGAACTGCCCCCCAAAGCTGTAGCAT
                    3440 CTGAGGAGAATGTGCGTGGCTCCTATAACTCAAGTAATAACTTCCAGCAACCTTTAACAT
                                                                                                                                                                            1018 CACGAGCAGAGGTGTGCCCTTGGGAGTTTGAGACCCCAGCTCAACCAAATGCTGGAAGAA
                                                                                                                                                                                                                                      CACGAGCAGAGGTTTGTCCTTGGGAGTTTGAGACCCCCAGCTCAACCAAATGCTGGAAGAA
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HTG: HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP
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ORGANISM
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KEYWORDS
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Db 188329 CAGGATGAACTGAAAAACTCTATGCTCAGTTAGAAATATACAAACGTAAAAAGATGATC 188388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2263 ATGAGACGCATTACGGAGATCCCAGAGACAGTCAGCCGGCAGTGCTCTAAAGAGGACAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGGGCGCCGACCATGGCACAGCCAAAGGCACTGCCCTCATCAGGAAGAACCCCCCAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTTCAGGGAACACAGGGAAATCCAAGGAGAGACCCTGAAAAACCGAGTCTTCTCACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAGAAATCCCACAGCACTTATGACCACGTGAGAGCCAAACGGAAGAGTCCAGTAGCCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAAAACTAACACAAAAACTAAAAGAAGACAGCGAGGCTGAGTCCACGGAGTGGGTGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGGTGTGCAAGTCAGCAAGCGCTCACAACCTCAGCTCAGAGAAAAAACTGGGCACCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 209802;
15336 15435: gap of 100 bp 15436 78237: contig of 62802 bp in length 78238 78337: gap of 100 bp 100 bp 80886 80985: contig of 2548 bp in length 80886 80985: gap of 100 bp 80986 209802: contig of 128817 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              400 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28.1%; Score 1026.6; DB 2; Length 81.3%; Pred. No. 7.7e-218; stive 0; Mismatches 264; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11198 - 15335 - 7 hote" assembly_fragment:00044 fragment_chain:1" 15436 . 78237 / note" assembly_fragment:00911 fragment_chain:1" 80883 . 80883 . 80883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380883 . 380880 . 380883 . 380880 . 380883 . 380883 . 380883 . 380883 . 380880 . 380880 . 380880 . 380880 . 38
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80986. .209802
/note="assembly_fragment:00556"
a 40593 c 41610 g 62105 t
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1. .11097
/note="assembly_fragment:00793
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus'
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
1. .209802
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                           Submitted (15-AUG-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assembly program: XGAP4, version 4.5
Sequencing vector: plasmid: L08752; 100% of reads
Chemistry: Dye-terminator Bib Dye; 100% of reads
Consensus quality: 90261 bases at least Q40
Consensus quality: 99226 bases at least Q30
Consensus quality: 104490 bases at least Q20
Insert size: 108717; sun-of-contigs
Consensus consensus quality: 104490 bases at least Q20
Insert size: 108717; sun-of-contigs
Quality coverage: 1.84x in Q20 bases; sum-of-contigs Quality
coverage: 1.42x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 25 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                  On Aug 27, 2000 this sequence version replaced gi:9926667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 16707; gap of 100 bp 20159; contig of 3452 bp in length 60 20259; gap of 100 bp 60 23641; contig of 3382 bp in length 642 23741; gap of 100 bp 62 27399; contig of 3658 bp in length 60 27499; gap of 100 bp 62 27499; gap of 100 bp 63658 bp in length 63658 bp 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 bp of 3330 bp in length 100 bp of 3308 bp in length 100 bp of 6782 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84: gap of 100 bp
5405: contig of 3821 bp in length
05: gap of 100 bp
56282: contig of 3777 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27499: gap of 100 bp
32754: contig of 5255 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       p of 100 bp contig of 2710 bp in length p of 100 bp contig of 4826 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oof 100 bp contig of 3431 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2287: contig of 2287 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 bp
5608 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         00: gap of 100 bp
68131: contig of 4831 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32854: gap of 100 bp
35240: contig of 2386 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .---- Summary Statistics
                              HTG; HTGS_PHASE1; HTGS_CANCELLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2288 2387; gap of 2388 6417; gap of 6318 6417; gap of 100 6418 9725; contig of 39726 9825; gap of 100 9826 16607; contig of 67
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43758: ~
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59669: con+
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63200: cont
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   GI:9930957
                                                                                                                                                                                                  (bases 1 to 111117)
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AL358932.3
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                              KEYWORDS
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ORGANISM
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TITLE
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                                                                                                                                                                                                  REFERENCE
   VERSION
                                                                                                                                                                                                                                                                                                                                                                                                     COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens chromosome 10 clone RP11-395P8, *** SEQUENCING IN PROGRESS ***, 25 unordered pieces.
Db 188869 CGTACATCTATGTTACAGAAATCTCTCAGTGTCATTGCAAGTGCCAAGGAGAAGACACTT 188928
                                                                                                                                                                                                                                                                                                                                                                   ------TCCCAAACTCCGGTCACATGGAGGAGCCAAGAAAGCCCCAGAAATCTGGG 189090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DD 189751 GCTTTAAGTGCAAATAAGATACCAGGGCCTCAGAAATAGGAAGTCTGGGACACTTTCAAA 189810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189390
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                                                                                                                           188929 GGCCTGGCTGGCAAAACCCAGACTTTAGTTATGGAAGACCGAGCTAAGTCCCAGAAA---
                                                                                                                                                                                                                                    188986 ---CCAAAAAGATAGAGACCATCAGGAAGTACTCAAATTCAGATAATGTAGAGACTA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     189211 ACCCCTGGTCCTATGCCTTCAGAGCTCAAAAACTCGGTATCAATCGCAGCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             189331 ACTGAAGGTCTCTACCAAGCCAATCACAAGAGCATAGACAAGACAGAGGTGTGCCCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 189511 GGGCAATATGAAGAACTGCCCCACAAAGTCGTAGCACCAAAAGTAGAAATGAAAATCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AACCAAATAGGACACCAGGAAAAAAAAGACATCTTCTTCTGAGGAGAATGTGCGTGGCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGATTAGCTGGGAAAACCCAAAACAGCAGGTGTGGAAGAACGCACTAAATCCCAGAAACCT
                                                                                                                                                                                                  TTGCCAAAAGATAAAGAGACAAACAGAAATCACTCAAATTCTGATAACACAGAGACTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTATGAAACAACAAGGGTCAACCCCACCACTGCCAATTCTGACCTGAACCCAGGCACC
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6823 70678: contig of 2447 bp in length 70679 70778: gap of 100 bp 72875: contig of 2097 bp in length 72876 72975: contig of 20097 bp in length 72876 72975: gap of 100 bp 72976 79043: contig of 6068 bp in length 7904 79143: gap of 100 bp 88144 88243: gap of 100 bp 88244 91655: contig of 9000 bp in length 91655 91784: gap of 100 bp 91755 102397: contig of 10643 bp in length 102398 102497: gap of 100 bp 100 bp 106285 111177: contig of 4833 bp in length.
                                                                                                                                                                                                                                                                                                                          15 111117: contig of 4833 bp in length. Location/Qualifiers
131: gap of 100 bp

10708: contig of 2447 bp in length

778: gap of 100 bp

72875: contig of 2097 bp in length
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1. .2287
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52506. .56282
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59770. .63200
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/note="assembly_fragment:00421"
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43859. .48684
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                  ture 91755. 102397.
/note="assembly_tragment:00573"
ture 10498. 106184
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ture 106285. 111117
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32506 a 20474 c 20158 g 35546 t 24
        'note="assembly_fragment:00562"
                                                                                                                     Query Match 24.8%; Score 903; DB Best Local Similarity 100.0%; Pred. No. 2.6 Matches 903; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (18-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, Cabomitted (18-SEP-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerquest@sanger.ac.uk

on Sep 19, 2001 this sequence version replaced gi:14586034.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality) as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSPROT; Tr:, TREMBL; WP; WORNEPP; Information on the WORNEPP that we have a subsequenced and the sequenced and the sequenced on the WORNEPP that we have a subsequenced and the sequenced on the WORNEPP that we have a subsequenced and the sequenced on the WORNEPP that we would be a subsequence on the worner and the sequenced on the worner and the sequence of the worner and the sequenced on t
                                                                                                                                                                                                                               163680 bp DNA linear PRI 18-SEP-2001 sequence from clone RP11-80K21 on chromosome 10, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 happing Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr10 RP11-80K21 is from the library RPCI-11.1 constructed by the group of Pleter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata, Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence is the entire insert of clone RP11-80K21 The true left end of clone RP13-99J21 is at 118860 in this sequence. The true right end of clone RP11-165A20 is at 18977 in this sequence. Location/Vaullifiers
84243 TGGCTGGTTACTCTTTCCTCTGCCATCTACGGGTTGCAGCCTAACCTGGTCCCGGAATTC 84302
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/note="match: STS: Em:HSJ167G10"

complement(71592. .71705)

/note="match: STS: Em:AL593168"

complement(71616. .71705)

/note="match: STS: Em:AU026983"
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complement(69918. .70348)
/note="match: STS: Em:G60781"
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VECTOR: pBACe3.6
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/db_xref="taxon:9606"
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37064. .37097
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Mammalia, Eutheria, Primates,
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ALI39821.9 GI:15705163
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Direct Submission
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                                                                                                                                                                                                                                                       Human DNA sequence.
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97379 AAGGGAAAGCCGCACGCCCAGCCGGTCGAGCCTCTGCCTCGGACTCCTCGGCTCCC 97438
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0
                                                                                  Length 163680;
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                                                                                                   100.0%; Pred. No. 2.7e-190; ive 0; Mismatches 0;
                                                                                     Score 903; DB 9;
                 /evidence=not_experimental 32541 c 33029 g 52645 t
/note="CpG island"
                                                                                     24.88;
                                                                                   Query Match 24.8
Best Local Similarity 100.
Matches 903; Conservative
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Rattus,

Rat
ACU94823 174215 bp DNA linear HTG 20-DEC-2001 Rattus norvegicus clone CH230-5J17, *** SEQUENCING IN PROGRESS ***, 61 unordered pieces.
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Direct Submission
Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:15624659.
                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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------ Project Information
Center project name: GBLR
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Rattus norvegicus
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HTG; HTGS_PHASE1.
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NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 61 contigs. The true order of the pieces is not known and their order in this sequence record is
                  Consensus quality: 152461 bases at least Q40 Consensus quality: 154423 bases at least Q30 Consensus quality: 163424 bases at least Q20 Estimated insert size: 155278; sum-of-contigs estimation Quality coverage: Ox in Q20 bases; agarose-fp estimation Quality coverage: 2.6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Assembly program: Phrap; version 0.990329First call to
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AC109216 163199 bp DNA linear HTG 28-APR-2002
Mus musculus clone RP23-390E1, WORKING DRAFT SEQUENCE, 13 ordered
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 16905 AGGGGGAAGCACGGTCAGCAGCTGCCGCAGCCTCTGCCCCGGACCCCTCTATTCCC 16846
                                                                                                                                                            16245 AGCCATGTCAAGTGGTCTCCACCTTTTCTGGAGTGCGAGAATGGGAGTTACAAGCCCGGG 16186
                                                                                                                                                                                                                                                                            16305 CAGGGGCCACGGGGCCTGGGCCACAGCTGGCGCGCAGGGATGGGCTTGGCGGGACAGG 16246
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                                                                                                     CAGGGCCCCGGGGCCTGGGCCACAGCTGGCGGCGCAAGGACGGCTCGGCGGGCACAAG
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                               TGGAGCCGCTCCACCGATGGCACCATCTTGGCGCAGAAACTCGCCGAGGAGGTGCCCATG
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AC109216.3 GI:20336087
HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FÜLLTOP.
Mus musculus.
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ITLE JOURNAL REFERENCE

AUTHORS

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Brown, A. Camarrata, J. Campoplano, A. Chango J. Chazgo, B. Brrown, A. Cannarata, J. Campoplano, A. Chango, J. Chargo, J. Chango, J.
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TITLE JOURNAL

MMENT

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onsists of 13 contigs. Gaps between the contigs are represented as runs of N. The order of the pleces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1229 others
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                                            GTGTGGAGCCTTCTGGAGGCGAGCCCAGCATCTCCCGGGCGGCGCCATCACCTTCAGCACC
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 Length 163199
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Score 730.2; DB 2;
Pred. No. 8.7e-152;
0; Mismatches 108;
20.0%;
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Search completed: February 15, 2003, 10:15:47 Job time : 15667 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			Description						ABV17708 Human prostate exp				
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			re Match Length DB I			7148	1800	368	398	470	182	83	705
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		2		103	21	AAA51616	HIV gp41 coding re
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		;	•	28	22	AAI58148	Human polynucleoti
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The present cDNA sequence encodes human G-protein coupled receptor (GPCR) which is a 7 transmembrane protein of G-protein coupled receptor (GPCR) super family. NGPCR is expressed in hypothalamus, focal brain, brain, cerebellum and testis. NGPCR spans the cellular membrane and is involved in signal transduction pathways. Human NGPCR is useful for treatheng obesity, inflammation, immune disorders, diabetes, heart and coronary disease, metabolic disorders and cancer. NGPCR s are also used as reagents in assays for screening compounds that are useful in the therepseutic treatment of physiclogical and behavioural disorders. NGPCR is useful for identifying compounds that modulate NGPCR gene expression and/or gene product activity. NGPCR DNA is also useful for the diagnostic and prognostic evaluation of disorders related to NGPCR function.

CN Nucleotide constructs encoding functional NGPCR and mutant NGPCR variants are used in gene therapy. NGPCR probes are also useful for the interval of the contraction and validation of novel molecular targets for a contraction.
                                                                                                          isolated polynucleotides encoding human G protein coupled tor (NGPCR), useful as probe and for treating disease involving detecting mutant NGPCR or abnormally expressed NGPCRs for
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Sequence 3648 BP; 969 A; 971 C; 917 G; 791 T; 0 other;

ö 180 180 240 GCTGTTGGCGCCAGCCGCGACCCCCAAGGACGGCCGGATTCCCCTCGAGAGAGGACCCCG 120 120 300 300 360 360 420 480 540 Gaps 9 9 AAGGGGAAGCCGCACCCCAGCAGCCGGGTCGAGCCTCTGCCTCGGACTCCTCGGCTCCC TGGAGCCGCTCCACCGATGGCACCATCTTGGCGCAGAAACTCGCCGAGGAGGTGCCCATG GACGTGGCCTCTTACCTCTACACCGGGGACTCCCACCAGCTGAAGCGAGCCAACTGCTCC CAGAGCAATAAGTCGCGGGAGCAGAACTTGCAGGACGACGACGACGTGGATTGGTACCAGGCGCTG TCCTTGCACCGGCGCTGGACACACACACACGCCCACCAACTTCCTCAACGTGATGCTG GTGTGGAGCCTTCTGGAGGGCGAGCCCAGCATCTCCCGGGCGGCGGCCATCACCTTCAGCACC GATTCGCTGTCCGCACCGGCCCCACAGGTCTTCCTCCAGGCCACGCGCGAGGAGAGCCGC GACGTGGCCTCTTACCTCTACACCGGGGACTCCCACCAGCTGAAGCGAGCCAACTGCTCC GGCCGCTACGAGTTGGCGGGCCTGCCGGGGAAGTGGCCAGCCCTGGCCAGCGCGCACCCC TCCTTGCACCGGGCGCTGGACACACTGACACGCCCACCAACTTCCTCAACGTGATGCTG CAGAGCAATAAGTCGCGGGAGCAGAACTTGCAGGACGACCTGGATTGGTACCAGGCGCTG 3648; ; 0 Length Indels 22; ; DB 0%; Score 3648; 0%; Pred. No. 0; 0; Mismatches 100.0%; 100.0%; Conservative Best Local Similarity Matches 3648; Conserv Match 19 61 121 121 181 181 241 241 301 361 301 361 421 421 481 541 181 g ò g ò 8 음 δ 유 δ a ο QQ ò Db δ g ò

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Human; G-protein coupled receptor; NGPCR; gene therapy; cancer; diabetes; inflammation; immune disorder; heart disease; obesity; coronary disease; 3180 3180 3240 3360 3480 2940 3000 3000 3060 3120 3120 3300 3420 3420 CAAACAGCAGGTGTGGAAGAACGCACTAAATCCCAGAAACCTTTGCCAAAAGATAAAGAG 2820 ATTITGGAAGAIGAGAAGCTITIGAITICCAAGACTCCCAGTICCCCAGAGAGGGCAAAA 3300 TCCAATCAGAAGCGCATAGATAAGGCTGAAGTATGCCTTTGGGAGAGCCAAGGCCAGTCC GAAAAAAAAGACATCTTCTTCTGAGGAGAATGTGCGTGGCTCCTATAACTCAAGTAATAAC ACTTTTTCCTTAAAGGAGAAATCTCACCACAAGCCTAAGGCAGCTGAGGTTTGTCAGCAA CAACCAAATGCTGGAAGAAGTGTAGCTTTACCTGCCTCTTCTGCTCTAAGTGCAAATAAG ACAAACAGAAATCACTCAAATTCTGATAACACAGAGAGTCTAAAGATCCTGCCCCCAAAAC TCAAATCCTGCGGAGGAGCCAAGAAGCCTCAGAAATCTGGGATTATGAAACAAAGG TTTGACATTGGGGAGGTGTCTCCTTGGGAGGTTTATGACCTGACCCCTGGTCCTGTGCCT TCAGAATCAAAAGTTCAAAAAGCACGTATCTATTGTGGCTTCTGAAATGGAGAAAAACCCC CCCCCCAAAGCTGTAGCATCAAAAACAGAGAATGAAAATCTCAACCAAATAGGACACCAG TTCCAGCAACCTTTAACATCACGAGCAGAGGTTTGTCCTTGGGAGTTTGAGACCCCAGCT ATAGCAGGCCTAGGAAAGAAGAACTCTGGGATAGTTTTAAAGTGTAG 3648 Human G-protein coupled receptor (NGPCR) cDNA. BP. AAD12294 standard; cDNA; 7148 (first entry) 16-OCT-2001 AAD12294; 2761 2821 2821 2881 2881 2941 3001 3061 3061 3181 3181 3241 3241 3301 3301 3361 3361 3421 3421 3481 3481 3541 3541 3601 3601 2941 3001 3121 2761 3121 RESULT 2
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physiological disorder; therapeutic; drug screening; behavioural disorder; ss.
metabolic disorder; prignal transduction;
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Homo sapiens

WO200157086-A2

09-AUG-2001

01-FEB-2001; 2001WO-US03648.

2000US-0180414. 04-FEB-2000;

(LEXI-) LEXICON GENETICS INC

Hilbun Donoho G, WPI; 2001-488870/53

Novel isolated polynucleotides encoding human G protein coupled receptor (NGPCR), useful as probe and for treating disease involving GPCR, detecting mutant NGPCR or abnormally expressed NGPCRs for diagnosing disease

Disclosure; Page 71-73; 73pp; English

The present invention relates to human G-protein coupled receptor (NGPCR) which is a 7 transmembrane protein of G-protein coupled receptor (GPCR) super family. NGPCR is expressed in hypothalamus, focal brain, brain, cerebellum and testis. NGPCR spans the cellular membrane and is involved in signal transduction pathways. Human NGPCR is useful for treathent obseity, inflammation, immune disorders, diabetes, heart and coronary disease, metabolic disorders and cancer. NGPCR are also used as reagents in assays for screening compounds that are useful in the therapeutic treatment of physiological and behavioural disorders. NGPCR is useful for identifying compounds that modulate NGPCR gene expression and/or gene product activity. NGPCR DNA is also useful for the diagnostic and prognostic evaluation of disorders related to NGPCR function.

C Nucleotide constructs encoding functional NGPCR and mutant NGPCR variants are used in gene therapy. NGPCR probes are also useful for the identification, selection and validation of novel molecular targets for dentification. receptor and 3' drug discovery. The present sequence is human G-protein coupled (NGPCR) cDNA containing coding sequence with the surrounding 5' regions drug

BP; 2014 A; 1655 C; 1608 G; 1870 T; 1 other; Sequence 7148

ä Gaps 113; Length 7148; Indels DB 22; ö 0; Mismatches Score 3525; Pred. No. 0; 96.6%; 97.0%; Conservative Best Local Similarity Matches 3648; Conserv uery Match

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- 180 AAGGGGAAGCCGCACCCAGCAGCCGGTCGAGCCTCTGCCTCGGACTCCTCGGCTCCC 549 121 g ò
- 240 AAGGGGAAGCCGCACCCAGCAGCCGGGTCGAGCCTCTGCCTCGGACTCCTCGGCTCC TGGAGCCGCTCCACCGATGGCACCATCTTGGCGCAGAAACTCGCCGAGGAGGTGCCCATG 181

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1088 1328 1028 840 AAAGGCCTAGGATTCGTTCTTGGAGCCTATGAGTGCATTTGCAAAGCAGGATTCTATCAT 1508 TTCTGTGCTGATGACAGCCCATGCTTCGTCCAGGAAGATAAGTATTTACGACTTGCCATC 1260 900 GGCCGCTACGAGTTGGCGGCCTGCCGGGGAAGTGGCCAGCCCTGGCCAGCGCGCACCCC 788 ATCCTGCTCCAAGACCTGTCCTCCTCCGCACCCCACGCCAACGCCAACTCTGGAGACC TCCTTGCACCGGGCGCTGGACACACTGACACGCCACCAACTTCCTCAACGTGATGCTG CAGAGCAATAAGTCGCGGGAGCAGAACTTGCAGGACGACCTGGATTGGTACCAGGCGCTG GTGTGGAGCCTTCTGGAGGGCGAGCCCAGCATCTCCCGGGCGGCCATCACCTTCAGCACC GATTCGCTGTCCCCACCGGCCCCACAGGTCTTCCTCCAGGCCACGCGCAGGAGAGACCGC ATCCTGCTCCAAGACCTGTCCTCCGCACCCCACCTGGCCAACGCCACTCTGGAGACC GAGTGGTTCCACGGCCTCCGGCGCAAGTGGAGGCCCCCACTTACACCGCGCCGCGCCCCAAT CAGGGGCCCCGGGGCCTGGGCCACAGCTGGCGGCGCAAGGACGGGCTCGGCGGGGACAAG AGCCACTTCAAGTGGTCTCCGCCTTATCTGGAGTGCGAGAACGGGAGTTACAAGCCCGGG TGGCTGGTTACTCTTTCCTCTGCCATCTACGGGTTGCAGCCTAACCTGGTCCCGGAATTC AGGGGTGTCATGAAAGTTGACATAAATCTTCAGAAAGTGGACATTGACCAATGCTCAAGT GATGGCTGGTTTTCAGGAACTCATAAATGCCACCTCAACAATTCAGAGTGTATGCCAATT AAAGGCCTAGGATTCGTTCGTTGGAGCCTATGAGTGCATTTGCAAAGCAGGATTCTATCAT CCTGGAGTCTTACCAGTGAACAACTTTCGGAGAAGGGGTCCGGATCAGCATATTTCAGGA ATCTCCTTCCAAGGCCTGTGTATGCTGCTCGACTTCGTTAGCATGCTGGTGGTCTACCAC TTTCGCAAAGCAAAGAGCATCCGGGCATCGGGCCTTATCCTGTTGGAAACGATCCTTTTT GGATCTCTGCTCCTATACTTTCCAGTTGTTATTTTGTACTTTGAGCCAAGCACATTTCGC 1029 1089 1149 1209 1389 1449 1081 1509 1141 1809 361 789 421 481 606 541 696 601 721 781 1269 1329 1021 1569 1201 1629 1261 1689 1321 1749 1381 661 841 901 961 Db g QQ αq q Вb Db QQ qq g pp ò ŏ g Ω ٥y δ δy ò ò ò g ò à οy δ g οy g g δy g οy q δy ò

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561 989	atgactggccgacggtcatgaggatgctggcagtaatactcttggtagtgttttggttt 1620 
621 049	CTCATTGGCTGGACTTCATCTGTGTGCCAGAATTTGGAGAAACAGATTTCACTTATTGGC 1680 
1681	CAGGGAAAACATCCGATCACCTCATCTTCAATATGTGCCTCATTGACCGCTGGGACTAC 1740 
1741 2169	ATGACAGCAGTTG 1753
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229	CATTACAACTGACTTCTTAAAAGTCTTGCCAGACTCTTTAGTAAAGCCTAAACTAATCT 2288
1754 2289	CTGAATTTTATTCTCTCTTGTGGGGTGTTATCTCTGCTATGCAGTGCGGACAG 1807 
808 349	TCCCATCGCATTCCATGAGCCCCGCTATATGCCTGTTGCAGTTCACAATGAGCTCATCA 1867 
409	TCTCTGCTATATTCCATACAATTAGATTTGTTCTTGCCTCAAGACTTCAGTCTGATTGGA 1927 
928	TGTTGATGCTGTATTTTGCACATACTCATTTGACTGTGACAGTCACCATTGGGTTGCTTT 1987 
ω σ <sub>0</sub>	TGATTCCAAAGTTTTCACATTCAAGCAATAACCCACGAGATGATAGCTACAGAAGCAT 2047 
048 589	ATGAGGATGAGCTAGACATGGGCCGATCTGGATCCTACCTGAACAGCAGTATCAATTCAG 2107 
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2228	agcegtgctcgaagaagegcctagetcettccatcatgagacecattacggacatcccag 2287 
288	AGACAGTCAGCCGGCAGTCCTCTAAAGAGGACAAAGGAGGCGCCGACCATGGCACAGCCA 2347 
α σ <sub>1</sub>	AAGGCACTGCCCTCATCAGGAAGAACCCCCCAGAGTCTTCAGGGAACACAGGGAAATCCA 2407 

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Nucleotide constructs encoding functional NGPCR and mutant NGPCR variants are used in gene therapy. NGPCR probes are also useful for the
                                                                                                                                                                                                                                                                                                                         Human; G-protein coupled receptor; NGPCR; gene therapy; cancer; diabetes; inflammation; immune disorder; heart disease; obesity; coronary disease; metabolic disorder; physiological disorder; therapeutic; drug screening; signal transduction; behavioural disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated polynucleotides encoding human G protein coupled receptor (NGPCR), useful as probe and for treating disease involving GPCR, detecting mutant NGPCR or abnormally expressed NGPCRs for
4029 AACCTITAACATCACGAGAGAGATTGTCTTGGGAGTTTGAGACCCCAGCTCAACCAA
                                                         4089 AIGCIGGAAGAAGIGTAGCTTTACCTGCTCTTCTGCTCTAAGIGCAATAAGATAGCAGCAG
                                                                                                                                                                                                                                                                                               Human G-protein coupled receptor (NGPCR) coding sequence #2 cDNA
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/product= "Human G-protein coupled receptor"
                                                                                                                   GGCCTAGGAAAGAAGATCTGGGATAGTTTTAAAGTGTAG 3648
                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                          BP.
                                                                                                                                                                                                       AAD12293 standard; cDNA; 1800
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     DB 22;
                                     16;
Score 1756.4;
Pred. No. 0;
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 48.1%;
larity 99.1%;
Conservative
                     Local Similarity
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expressed sequence tag; EST; probe; chemotactic; proliferative; immunomodulatory; haemotacic; chemotinetic; analgesic; haemostatic; thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal; antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian; antiulcer; osteopathic; neuroprotective; noctropic; antiparkinsonian; cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine; autoimmune disorder; multiple sclerosis; allegic condition; insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer;
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            CCTGGAGTCTTACCAGTGAACAACTTTCGGAGAAGGGGTCCGGATCAGCATATTTCAGGA
                                                                                                                                                                                       CAGGGGAAAACATCCGATCACCTCATCTTCAATATGTGCCTCATTGACCGCTGGGACTAC
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                                                        CCTGGAGTCTTACCAGTGAACAACTTTCGGAGAAGGGGTCCGGATCAGCATATTTCAGGA
                                                                                                                TTCTGTGCTGATGACAGCCCATGCTTCGTCCAGGAAGATAAGTATTTACGACTTGCCATC
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sequence tags (SESTS), isolated from human, mouse, xenopus and rattices the segment of activities depending on the tissue sources. The SESTS can have a range of activities depending on the tissues they were isolated from. The activities depending on the tissues they were isolated from. The activities depending on chemothetic; proliferative; inamnomodulatory; haematopoietic; chemothetic; analgesic; haemostatic; thrombolytic; antinflammatory; cytostatic; antibacterial; antiducer; osteopathic; neuroprotective; notropic; antiparkinsonian; antipsoriatic; cerebroprotective; notropic; antiparkinsonian; antipsoriatic; cerebroprotective; anticonvulsant; and antidepressant. The SESTs can be used for gene therapy and in vaccines. The SESTs are useful as probes for the identification and isolation of full-length cDNAs and genomic DNA molecules which correspond to the SESTs. Proteins encoded by the SESTs are useful in assays for determining blological activity and raising antibodies. They may be useful for treatment of autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (multiple sclerosis, insulin dependent diabetes), allergic conditions (asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (Alzheimer's, Parkinson's, Huntington's disease, stroke), coaquilation disorders (haemophilia, thrombosis), inflammatory disorders (crohn's disease), tumours, bacterial, fungal or viral infections, depression and psoriasis. AAA3420 to AAA43425 represent linker variants which are given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (SESTS), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders
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                 central nervous system disorder; Alzheimer's disease; stroke;
Parkinson's disease; Huntington's disease; coagulation disorder;
haemophilia; thrombosis; inflammatory disorder; Crohn's disease;
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    burn; osteoporosis; osteoarthritis;
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                                                                               tumour; infection; depression; psoriasis; ss.
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cell deficiency;
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Matches 344; Conservative
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2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-229007P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABV47501 standard; cDNA; 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-FEB-2001; 2001WO-US05171.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schlegel R, Endege WO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-662795/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200160860-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-FEB-2000;
16-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABV47501;
  169
                                                                                               829
                                                                                                                                                                                                                                                                                       949 (
                                                                                                                                           82
                                                                                                                                                                                            889
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 6
ABV47501
                                         g
                                                                                             δ
                                                                                                                                           g
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                                                                                                                                                                                                                                      qq
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                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
199 AGGATGAGCTAGACATGGGCCGATCTGGATCCTACCTGAACAGCAGTATCAATTCAGCCT 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid molecule (I) comp a nucleotide sequence given in Tables 1-9 (ABV6010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful as a pharmacodyanamic or pharmacogenomic marker.
                                            6.6%; Score 240; DB 23; Length 398; 100.0%; Pred. No. 3.3e-55; ive 0; Mismatches 0; Indels
                                                                                                                                         Sequence 398 BP; 122 A; 82 C; 103 G; 91 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human prostate expression marker cDNA 17699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 2926-2927; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schlegel R, Endege WO, Monahan JE;
                                                                                                                                                                                                                                                                                                               ВР
                                                                                                                                                                                                                                                                                                             ABV17708 standard; cDNA; 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-MAX-2000; 2000US-189862P.
25-MAX-2000; 2000US-207454P.
09-JUN-2000; 2000US-211314P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-JUL-2000; 2000US-219007P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-FEB-2001; 2001WO-US05171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-FEB-2000; 2000US-183319P.
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Best Local Similarity 100.
Matches 240; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-662795/76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200160860-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (I) is also
                                                                                                                                                                                                                                                                                                                                                                                                        13-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-AUG-2001
                                                                                                                                                                                                                                                                                                                                                         ABV17708;
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
cancer in a patient;
(d) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
in a patient;

(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a patient;
(l) is also useful as a pharmacodyanamic or pharmacogenomic marker.

                                                                                                                                                                                                                                                                                                                                                                                                                             cancer; cytostatic; carcinogen; pharmacodyanamic marker;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                              261
           81
                                                             CAATGCTCAAGTGATGGCTGGTTTTCAGGAACTCATAAATGCCACCTCAACAATTCAGAG
                                                                                                                                                                                                 22 GGCGGGGACAAGAGCCACTTCAAGTGGTCTCCGCCTTATCTGGAGTGCGAGAACGGGAGT
                                              TACAAGCCCGGGTGGCTGGTTACTCTTTCCTCTGCCATCTACGGGTTGCAGCCTAACCTG
                                                                                                               GTCCCGGAATTCAGGGGTGTCATGAAAGTTGACATAAATCTTCAGAAAGTGGACATTGAC
                                                                                                                                                                                                                                                                                                                                                                                             prostate expression marker cDNA 47492.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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(multiple sclerosis, insulin dependent diabetes), allergic conditions (sathma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers, osteoporosis, osteoarthritis, central nervous system disorders (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation disorders (haemophilla, thrombosis), inflammatory disorders (crohn's disease), tumours, bacterial, fungal or viral infections, depression and psoriasis, AAA43420 represent linker variants which are given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1529 TTCTTTCACGAACGGCTCAACGAATTCCATATATGACTGGCGGACGGGTCATGAGGATGC 1588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1589 TGGCAGTAATACTCTTGGTAGTGTTTTGGTTTCTCATTGGCTGGACTTCATCTGTGTGCC 1648
tissue sources. The SESTs can have a range of activities depending on the tissues they were isolated from. The activities include: chemotractic; proliferative; immunomodulacory; haematopoletic; chemotinetic; antibacterial; antifundal; antiviral; antianflammatory; cytostatic; antibacterial; antifundal; antiviral; antianflammatory; antianathmatic; vulnerary; antibleer; osteopathic; neuroprotective; anticonvulsant; and antibacherssant. The SESTs can be used for gene therapy and in vaccines. The SESTs are useful as probes for the identification and isolation of full-length cONAs and genomic DNA molecules which correspond to the SESTs. Proteins encoded by the SESTs are useful in assays for determining biological activity and raising antibolies. They may be useful for treatment of autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 TGGCAGTAATACTCTTGGTAGTGTTTTGGTTTTTGGTTTGTCATTGGCTGGACTTCATCTGTGTGGCC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1649 AGAATTTGGAGAAACAGATTTCACTTATTGGCCAGGGGAAAACATCCGATCACCTC 1704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 TICGGCCAAAGAGGCCTAATIGAATICCATATATGACTGGCGGACGGGTCATGAGGATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    124 AGAATTTGGAGAAACAGATTTCACTTATTGGCCAGGGGAAAACACCCGGATCACCTC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 182 BP; 46 A; 36 C; 49 G; 51 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted protein 5' EST, SEQ ID NO: 12960.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 156.8; DB 2 Pred. No. 1.3e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.38;
93.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-FEB-2000; 2000EP-0200610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC08885 standard; cDNA; 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0122487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 164; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EP1033401-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC08885;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Loral e
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AAC08885
        g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expressed sequence tag; EST; probe; chemotactic; proliferative; immunomodulatory; haematopoietic; chemotactic; analgesic; haemostatic; thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal; antiviral; antiadiabetic; antiasthmatic; vulnerary; antiparkinsonian; antiulcer; osteopathic; neuroprotective; nootropic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expressed sequence tags (SESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA41261 to AAA43419 represent specifically claimed secreted expressed sequence tags (sESTs), isolated from human, mouse, xenopus and rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  949 CAATGCTCAAGTGATGGCTGGTTTTCAGGAACTCATAAATGCCACCTCAACAATTCAGAG 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cerebroprotective; anticonvulsant; antidepressant; gene therapy; vaccine; autoimmune disorder; multiple sclerosis; allergic condition; insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer; lymphoid cell deficiency; burn; osteoporosis; osteoarthritis; central nervous system disorder; Alzheimer's disease; stroke; Parkinson's disease; Huntington's disease; coagulation disorder; haemophilia; thrombosis; inflammatory disorder; Crohn's disease;
                                                                                                                                                                                                                                                              888
                                                                                                                                                                                                                                                                                                                                                                                         249 CAATGCTCAACTGATGGCTGGTTTTCAGGAACTCATAAATGCCACCTCAACAATTCAGAG 308
                                                                                                                                                                                                      69 GGCGGGGACAAGAGCCACTICAAGIGGICICCGCCTIAICIGGAGIGCGAGAACGGGAGI 128
                                                                                                                                                                                                                                                                                                            129 TACAAGCCCGGGTGGCTGGTTACTCTTTCCTCCCATCTACGGGTTGCAGCCTAACCTG 188
                                                                                                                                                                                                                                                                                                                                                            889 GTCCCGGAATTCAGGGGTGTCATGAAAGTTGACATAAATCTTCAGAAAGTGGACATTGAC 948
                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteins, comprising secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mouse; xenopus; rat; secreted expressed sequence tag; SEST;
                                                                                                                                                        769 GCCGGGGACAAGAGCCACTTCAAGTGGTCTCCGCCTTATCTGGAGTGCGAGAACGGGAGT
                                                                                                                                                                                                                                                         829 TACAAGCCCGGGTGGCTGGTTACTCTTTCCTCTGCCATCTACGGGTTGCAGCCTAACCTG
                                                                                                                                                                                                                                                                                      ς;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Evans
                                                        Length 470;
                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LaVallie ER, Collins-Racie LA,
Sequence 470 BP; 145 A; 106 C; 120 G; 99 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted expressed sequence tag SEQ ID NO:323.
                                                  6.6%; Score 240; DB 23;
1larity 100.0%; Pred. No. 3.6e-55;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumour; infection; depression; psoriasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated polynucleotides, and encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 243; 618pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA41583 standard; cDNA; 182 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US24205.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GEMY ) GENETICS INST INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McCoy JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Treacy M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-317937/27.
                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200021990-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-OCT-1999;
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                                                                                Best Local Sim
Matches 240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-APR-2000
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Merberq D,
                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAA41583;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Merberg
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AAA41583
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12; Indels

Length 182;

DB 21;

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mutation detection; ss
                                                                                                                                        Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                GCTTTT 1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         546 CATCTT 551
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                                The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. S' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                     2263 ATGAGACGCATTACGGAGATCCCAGAGACAGTCAGCCGGCAGTGCTCTAAAGAGGACAAG 2322
                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster genomic polynucleotide SEQ ID NO 13678.
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                                                                                                                                                                                                                                                     Length 83;
                                                                                                                                                                                                                                                                            Indels
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2.2e-07;
                                                                                                                                                                                                                            Sequence 83 BP; 27 A; 19 C; 26 G; 11 T; 0 other;
          Claim 1; SEQ ID 12960; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                     1.8%; Score 64; DB 100.0%; Pred. No. 2.2 Live 0; Mismatches
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                                                                                                                                                                                                    expression and secretion vectors.
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2000US-0614150.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pharmaceutical; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-656860/75.
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11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                              61 GAGG 64
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specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1683 GGGGAAAACATCCGATCACCTCATCTTCAATATGTGCCTCCATTGACCGCTGGGACTACAT 1742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1923 TTGGATGTTGATGCTGTATTTTGCACATACTCATTTGACTGTGACAGTCACCATTGGGTT 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sixty six Drosophila Melanogaster G-protein coupled receptors (GPCR), useful in the treatment and diagnosis of GPCR-related conditions and for identifying GPCR modulators for use as insecticides -
insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
                                  discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL016175) and the encoded proteins (ABB57737-ABB27072).

The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306 GTTCACCTCGATGGAGGTCCTGTTCCTGGCCTGGGGGGTTCGCCTGTGCATCATGGTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1743 GACAGCAGTIGCTGAATITITATICCTCTIGIGGGGTGTITATCTCTGCTATGCAGTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GACAGTCCCATCGGCATTCCATGAGCCCCGCTATATGGCTGTTGCAGTTCACAATGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              366 GAAGGCGCCGTCGGAGTTCAACGAGAGCCGCTTCATCTCGATGGCCATCTACAATGAGTT
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                                                                                                                                                                                                                                                                                                                                          Length
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                                                                                                                                                                                                                                                                        Sequence 795 BP; 146 A; 250 C; 220 G; 179 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                      DB 23;
                                                                                                                                                                                                                                                                                                                                      Score 62.8; DB 23 Pred. No. 1.8e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS57193 standard; cDNA; 2010 BP
                                                                                                                                                                                                                                                                                                                                      1.7%;
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18-JUL-2000; 2000US-0618893.
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                                            The invention relates to sixty six novel isolated Drosophila melanogaster G-protein coupled receptors (GPCR). The GPCR proteins and nucleic acids are useful in the treatment and diagnosis of GPCR-related conditions. The GPCR proteins and nucleic acids are also useful for identifying modulators of GPCR proteins for use as insecticides. The mucleic acid can also be used to detect mutations in GPCR genes and gene expression products such as mRNA. AASS70702-AASS7032 represent D. melanogaster G-coupled protein receptor genomic and coding sequences of
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                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                   Length 2010;
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                                                                                                                                                                                                                              Sequence 2010 BP; 410 A; 590 C; 571 G; 439 T; 0 other;
                                                                                                                                                                                                                                                               Query Match
1.6%; Score 59.8; DB 22;
Best Local Similarity 43.8%; Pred. No. 2.1e-05;
Matches 445; Conservative 0; Mismatches 542;
            Page 275; 392pp; English
                                                                                                                                                                                             the invention.
                4;
                Claim
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     שיים באסומ חוסבו מנו detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL0156-ABL3051), expressed DNA sequences (ABL01676-ABL3051), expressed DNA
                                                                                                                                                           1229 TCCAGGAAGATAAGTATTTACGACTTGCCATCATCTCCTTCCAAGGCCTGTGTATGCTGC 1288
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                                                                                                                                                                                                                                                                                  1709 ACAAGACTCTGCGGCAGGACAATCCGCACATCAGTAAGCGACGAGGGACGAAGG 1765
                                                                                                                                                                                                                                                  2189 GAAAGAAGATGATCACAAACAACCCCCCCCCCGGAAAAAGCGGTGCTCGAAGAAGG 2245
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                                                          GATATGCCGGGCTCTGTCTGGGCGATCCGGACATTGGTGAGCTGACCATATCCGAAATGA
                                                                                                                          ATCCAGAGGACATTCGGGACGAGCTGAAAAAACTCTATGCCCAACTGGAAATATAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster genomic polynucleotide SEQ ID NO 35722.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 35722; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               542;
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11-JUL-2000; 2000US-0614150
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Cellulose synthase; cellulose production; increase yield;

angularis JP2000060568-A.

Vigna

98JP-0239998 98JP-0239998

26-AUG-1998; 26-AUG-1998;

29-FEB-2000

(MIZU/) MIZUNO K. (OJIP ) OJI PAPER CO.

WPI; 2000-342371/30. P-PSDB; AAY85179.

Gene encoding a subunit of cellulose synthase

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              GTATGTGGACTGTGCTGGACATACTGCTGGGCATTTTTACTTTTATGCATCGTTG
                                                                                                                                                                                       TGGGCACCATGGTCTTTGCCGTCATCTGCTACATGGCCGCCTTTACGGCCTCGTTGG
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                                                                                                               TTATTTTGTACTTTGAGCCAAGCACATTTCGCTGTATTCTCCTAAGATGGGCTCGTCTTC
                                                                                                                                  CCTCCATITCTITCCCGCATCCACCGAGCGCTGCTTCTGGAGCCCTGGCTTCGGGAGC
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                                                       CGGGCCTTATCCTGTTGGAAACGATCCTTTTTGGATCTCTGCTCCTATACTTTCCAGTTG
                                                                                                                                                                     TCGGTTTTGCTACTGTTTACGGAACTGTCACTCTCAAACTTCACAGGGTTTTGAAGGTGT
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A gene encoding a cellulose synthetic equipment - for the improvement in the amount of cellulose synthesised in a plant body

Claim 2; Page 14-21; 32pp; Japanese

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This sequence represents a gene encoding a subunit of the cellulose synthase complex of Vigna angularis. The invention relates to subunits cellulose synthetic equipment, that can be used to increase the amount cellulose synthesised by a plant. The proteins and genes encoding them can also be used to improve the properties of the cellulose being produced by a plant.
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                                                                                                                                                                                                                                                                      Length 10732;
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                                                                                                                                                                                                            Sequence 10732 BP; 3149 A; 1212 C; 2074 G; 2046 T; 2251 other;
                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                   1.5%; Score 56.4; DB 21;
Best Local Similarity 14.3%; Pred. No. 0.00049;
Matches 186; Conservative 481; Mismatches 625;
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        TCGGTGCCGTTGGTGTGCAAGTCAGCAAGCGCTCACAACCTCAGCTCAGAAAAACT 2673
                                                                     9648 AATHRGNSRRSRAASRYSAAVATHRGASNSRSRGTHRGYTHRYSGSRTHRRGGGYYSGRV 9707
                                                                                                            2913 GABATCTGGGATTATGAAACAACAAGGGTCAACCCCACCACTGCCAATTCTGACCTGAA 2972
                                                                                                                                                                                                                                                                               2973 CCCAGGCACCACCACCAGATGAAGGACAACTTTGACA--TTGGGGAGGTGTGTCCTTGGGAG 3030
                                                                                                                                                                                                                                                                                                                            GTTTATGACCTGACCCCTGGTCCTGTGCCTTCAGAATCAAAAGTTCAAAAGCACGTATCT 3090
                             RGYSYSYSGRSRCYSYSSRVAGYAASRASASNMTASASHVAGMTGYSAAVAVASRVAGYS 9647
                                                                                                                                          2793 CCAGAAACCTTTGCCAAAAGATAAAGAGACAAACAGAAATCACTCAAATTCTGATAACAC 2852
                                                                                                                                                                RCYSSRASHYSGYTHRVARGYTRGNASVAVAYSTHRGGNASNHSVATHRHSYSGYRASAS 9827
                                                                                               GAAGACTCTTGGATTAGCTGGGAAAACCCAAACAGCAGGTGTGGAAGAACGCACTAAATC
                                                                                                                                                                                                                                                 AGAGACTAAAAGATCCTGCCCCCCAAAACTCCAGAATCCTGCGGAGGAGCCAAGAAAGCCTCA
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                                                   GGGCA-CCCACGAACATCGATGTTACAGAAGTCTCTCAGTGTCATAGCAAGCGCCAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGACTCCAGTTCTCCCAGAGAGGGCAAAAGAGGAGGAACGGAGGTCAGCCTCGTGCAGCC
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Expression cassettes comprising a polynucleotide encoding antigenic type C human immunodeficiency virus (HIV) Gag or Env polypeptides are useful in DNA immunization, generation of packaging cell lines and production of Gag- and/or Env-containing proteins. Synthetic Env and Gag expression cassettes exhibit increased potency for induction of cytotoxic T-lymphocyte (CTL) responses by DNA immunization. Gag of HIV-1 self-assemble into non-infectious virus-like particles which are used as a matrix for the proper presentation of an antigen entrapped or associated to the immune system of the host.
                                                                                                                                                                                                                                                                                      Polynucleotide encoding antigenic type C HIV Gag polypeptide or a HIV Env polypeptide and the polypeptide useful for immunizing a mammal especially human against HIV
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Pred. No. 0.0019;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1035 BP; 189 A; 368 C; 327 G; 151 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 52;
                                                                                                                                                                                                                                                                                                                                                                                               Claim 16; Page 97; 113pp; English.
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                                                                                                                                                                                     Zur Megede
                                                                                                                              (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                       WPI; 2000-452401/39.
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30-DEC-1999;
                                                 31-DEC-1998;
01-SEP-1999;
                                                                                                                                                                                   Barnett S,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1898 AGAACCTGTGGAACTGGTTCAGCATCACCAACTGGCTGTGGTACATCATCATCATCA 1957
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Pred. No. 0.0033;
0; Mismatches 240; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2466 BP; 540 A; 870 C; 725 G; 331 T; 0 other;
            HIV gp160 coding region (nucleotides 82-2547).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 14; Page 95-96; 113pp; English.
                                                                                               Human immunodeficiency virus type C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.4%;
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99US-0152195
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Best Local Similarity 45.0
Matches 196; Conservative
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                                                                                                                                                                                                                                                                                     (CHIR ) CHIRON CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gag; expression cassette; antigenic; type C; HIV; Env; synthetic; DNA immunization; packaging cell line; antigen presentation; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HIV gp160 with signal sequence DNA (nucleotides 1-2547).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2547 BP; 556 A; 888 C; 753 G; 350 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            associated to the immune system of the host.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 15; Page 96-97; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human immunodeficiency virus type C.
                                                                                                                                                                                                                                                                         BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó;
                                                                                                                                                                                                                                                                     AAA51615 standard; DNA; 2547
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                                                                     2198 GCTACCACCGCCTGCG 2213
                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .,
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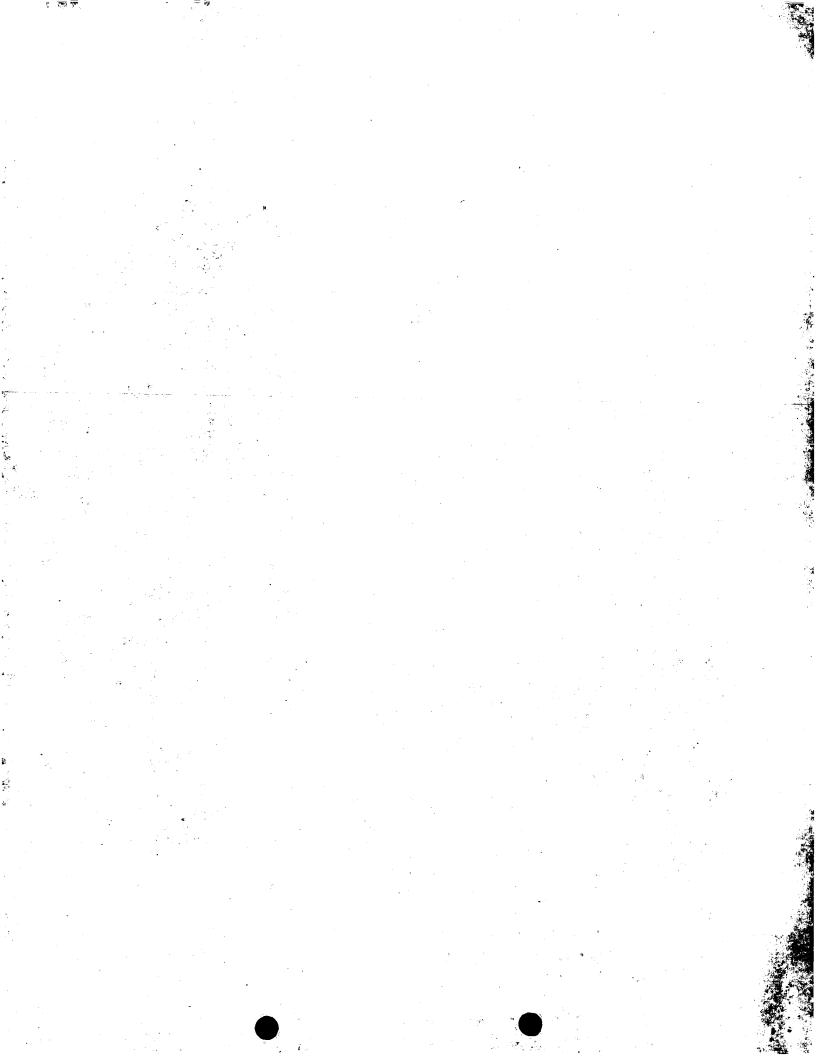
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1 (bases 1 to 628)

2 Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Ishii, Y., Ito, M., Kawai, J., Ohno, H., Koya, S., Matsuyama, T., Saito, R., Sakai, K., Sano, H., Sasaki, J., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., RIKEN Mouse ESTS (Arakawa, T., et al. 2001)

Inpublished (2001)

Cottact: Yoshinde Hayashizaki
Contact: Yoshinde Hayashizaki
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
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URL:http://genome-gsc.riken.go.jp,
Carninci.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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Konnoyer, Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara K., Tand Hayashizaki,Y.

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Computational Analysis of Full-Length Mouse CDNAs Compared with
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               Email: genome_res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayatsu,W., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazaki,Y., Muramatsu,M., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rappid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
'S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
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/dev_stage="adult"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="C630030A14"
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sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                                                                                                                                                                              Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length CDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="RIKEN full-length enriched, adult male corpora
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagl,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawal,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                            Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Saguences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
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/dev_stage="adult"
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Pred. No. 8.2e-112;
0; Mismatches 78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
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/clone="B230315M17"
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Best Local Similarity 87.6%;
Matches 549; Conservative
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BQ109073 628 bp mRNA linear EST 16-APR-2002 imagegc_8_2001/sno349bdrr81.yl NIH_MGC_94 Mus musculus cDNA clone IMAGE:5365177 5', mRNA sequence.
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This read has been produced as part of the I.M.A.G.E. Consortium
quality control effort. High quality sequence is defined as having
100 or more base pairs with a phred quality value of 20 or greater,
where a sliding window of 4 base pairs with a phred quality value
of 15 or greater marks the beginning and end of the sequence. For
information on obtaining this clone, please contact
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Kale, P. I., Harsch, T. J., Folta, P. A., Nelson, D. O., Sanders, C. G. and Prange, C. K.
Phe I. M. A. G. E. Consortium quality control effort: clone resequencing for verification Unpublished (2001)
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/organism="Mus musculus"
/do_xref="taxon:logo"
/do_xref="taxon:logo"
/clone="IMAGC_545177"
/clone_lib="NIH_MGC_94"
/tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/note="Organ:eye; Vector: pCMV-SPORT6; Site_1: Not!; Site_2: Sal1; Cloned unidirectionally; oligo-dT primed.
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                       268 CTCTGGTGCGAAGTCTCCTGGAGGTGAGCCCAGCATCTCCCGGGGGGGCGCCATCACCTTCA
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                                                                                     TGCTGCAGAGCAATAAGTCGCGGGAGCAGAACTTGCAGGACGACGTGGATTGGTACCAGG
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The I.M.A.G.E. Consortium
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Plate: LLAM11929 rov
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Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

202 c 167 g 130 t 1 others
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Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
                                                                                 Length 628
                                                                              Score 439.2; DB 14; Length
Pred. No. 2.9e-96;
); Mismatches 74; Indels
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High Throughput Sequencing Center
                                                                                                         0; Mismatches
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                                                                                12.0%;
86.7%;
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                                                                                                         Matches 483; Conservative
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Best Local 3
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GSS 30-AUG-1999
401 Queen Anne Avenue North, Seattle, WA 98109, USA
THE: (206) 616-3818
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3118 row: E oolumn: 19
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 554)
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                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=3118 Col=19 Row=E"
/clone_lib="CIT Approved Human Genomic Sperm Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACAAACAACCCCCACCTCCAGAAAAAGCGGTGCTCGAAGAAGGGGCCTAGGTCGTTCCATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 17; Length 508;
                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: sperm; Vector: pBeloBAC11; BAC E-Coli DH10B" 98 t 6 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 380.8; DB 17;
Pred. No. 5.2e-82;
0; Mismatches 13;
                                                                                                                                                               Seg primer: M13 Reverse
Class: BAC ends
High quality sequence stop: E
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tch 10.4%; al Similarity 96.4%; 407; Conservative C
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Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3868
Fax: (206) 616-3868
Email: yele-3887
E
                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 543)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACGS.6 vector is tech sites. 5 others
                                                                                                                                                  GSS 15-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACAACCCCCACCTCCAGAAAAAGCGGTGCTCGAAGAAGGGCCCTAGGTCGTTCCATCATG 2265
                                                                                                                                              AQ728799 543 bp DNA linear GSS 15-JUL-
HS_5464_B2_A11_T7A RPCI-11 Human Male BAC Library Homo sapiens
genomic clone Plate=1040 Col=22 Row=B, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RPCI-11 Human Male BAC Library"
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Pred. No. 4.2e-71;
0; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="Plate=1040 Col=22 Row=B"
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      510 GCTATCTATAGAGACAGCGAGGCTTATTC 539
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Location/Qualifiers
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GSS.
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Matches 368; Conservative
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KEYWORDS
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                                                                                                                                                                                         Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Mashington
401 Queen Anne Avonue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pleter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 1040 row: O column: 3
Seg primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pBACe3.6; Site_1: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
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Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAGATCCCAGAGACAGTCAGCCGGCAGTGCTCTAAAGAGGACAAAGAGGAGGGCGCCGACCA 2336
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                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="plate=1040 Col=3 Row=O"
/clone_lib="RPCI-11 Human Male BAC Library"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 others
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scanning the hum
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Konno, H., Atawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hizawa, T., Eukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hizawa, T., Enkiwa, J., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, T., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, K., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Saitch, H., Sattch, H., Sakai, C., Sato, K., Shibata, Y., Sungemoto, Y., Shinagawa, A., Shiraki, T., Sugabe, Y., Sugahara, Y., Suzuki, H., Tagawa, A., Takahashi, T., Yamanaxi, T., Yamoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yamanaka, T., Yamanatsu, M., Muramatsu, M., and Hayashizaki, Y. Sunki, H., Suzuki, H., Suzuki, H., Yoshida, K., Yoshida, K., Yoshino, RIKEN Mouse ESTS (Konno, H., et al.)

Londortory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute of Physical and Chemical Research (RIKEN)

The Institute of Physical and Chemical Research (RIKEN)

Tal: 81-45-503-9226
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URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Nishiyama.Y., Westover.A., Itoh,M., Nagaoka,S., Sasaki,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomatu,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BB354926 BIKEN full-length enriched, adult male corpus striatum Mus musculus cDNA clone C030003G02 3', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210 AAAACCTCGGGATGACTCCCTTAAAAACAAGGTCATGGTTTTGCCGAAGTCACTCAGC-- 153
                             2340 CACAGCCAAAGGCACTGCCCTCATCAGGAAGAACCCCCCAGAGTCTTCAGGGAACACAGG
  2100 CAATTCAGCCTGGAGTGAGCACAGCTTGGATCCAGAGGACATTCGGGACGAGCTGAAAAA
                                                                                                                                                                                          2220 CCAGAAAAAGCGGTGCTCGAAGAAGGGCCTAGGTCGTTCCATCATGAGACGCATTACGGA
                                                                                                                                                                                                                  GATCCCAGAGACAGTCAGCCGGCAGTGCTCTAAAGAGGACAAGGAGGGCGCCGACCATGG
                                                                                                                                                                                                                                                                                                                                                                                                            321 GATCCCAGAGACCATGCACATCCACCGGCAGTGCAGCCGAGAGACGACGCAGCGAGCACGG
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Autional Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: Kmita@nirs.go.jp
method:uni-directional sequence direction:sequenced from T3 primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha; Beloniformes; Adrianichthyidae; Oryziinae; Oryzias.
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290 GGCGCCGACCATGGCACAGTCAAATGCTCTGTCCTCATCAAGAAGAACCCCCCAGAGTCT 349
                                                                                                                                                                                       469
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                                                                                                                                                                                                                                                             470 CTCGAAAGCTCAGAGGAGGAGACATCAGACTATTGCACACTGTGATCCCTGTCGAGGAAA
                                                                                                                                         2446 AAATCCCACAGGCACTTATGACCACGTGAGAGACCAAACGGAAGAGTCCAGTAGCCTACCC
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Establishment of CDNA database of medaka, Oryzias latipes
Unpublished (2001)
Contact: Mita K
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ilarity 65.2%; Pred. No. 2.6e-43;
Conservative 0; Mismatches 189;
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/sex="female/male mixed"
/tissue_type="brain"
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/clone="br8300"
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173 c 185 g
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AUI71941.1 GI:12594012
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Oryzias latipes
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GSS; genome survey sequence.

Tetracdon nigroviridis.

Tetracdon nigroviridis.

Tetracon nigroviridis.

Bukaryota; Metazca; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Suteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetracdontiformes;

Tetracdontidae; Tetracdon.

[ bases 1 to 895)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,

Bernot, A., Fizames, C., Wincker, P., Brottler, P., Quetier, F.,

Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                       Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                        2 (bases 1 to 895)
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                  Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="G"
/note="Genoscope sequence ID : COAG207DA02LP1-end : T7"
/note="Genoscope sequence ID : COAG207DA02LP1-end : T7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (12-APR-2000)
This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="207B04"
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                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in
  Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 467-470 (1999) Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTTCTTGCCTCAAGACTTCAGTCTGATTGGATGTTGATGCTGTATTTTGCACATACTCAT 1956
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0; Mismatches 38; Indels
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/dev_stage="adult"
/lab_host="DH108"
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                                                                                                                                                                                                          /organism="Mus musculus"
/strain="C57BL/6J"
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/clone="C030003G02"
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Best Local Similarity 86.4%;
Matches 242; Conservative
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Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramotco, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii , Y., Ito, M., Kawai, J., Kojima, Y., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shinabata, K., Shinataki, R., Sakabe, Y., Suzuki, H., Tagawa, A., Takaku, A., Shiraki, T., Soqabe, Y., Suzuki, H., Tagawa, A., Takaku, A., Takaku, A., Takaku, A., Tayaku, A., Takaku, A., Tayaku, A., Takaku, A., Tayaku, M., Muramatsu, M., and Hayashizaki, Y.

RIKEN Encyclopedia of Mouse Full-length cDNAS (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIXEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
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UR.:http://genome.gsc.riken.go.jp,
UR.:http://genome.gsc.riken.go.jp,
Carnincl,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazaki,Y., Muramatsu,M., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNas to
prepare [Inl:-ength cDNA libraries for rappid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Wathiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
'S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
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Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Laboratorry for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
Tel: 81-45-503-922
Fax: 81-45-503-9216
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 356)
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/clone_lib="RIKEN full-length enriched, 16 days neonate
male diencephalon"
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                                                                                                483 AGTGCACCGAGTCCGTTCCTCTGGTCTGCAAGTCGGCCAGCGCTCATAACCTCTCGGCGG 424
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases I to 755)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinaya, A., Shiraki, T., Soqabe, Y., Suzuki, H., Taqami, M., Taqawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.,
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cerebellum Mus
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Normalization and subtraction of cap-trapper-selected cDNs to prepare full-length cDNs 1 libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi, K., Pujiwake, S., Inoue, K., Togawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2001)
On Jul 6, 2000 this sequence version replaced gi:8948735.
Contact: Yoshinde Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
                                                                     dev_stage=16 days neonate, sex=mixed),
(tissue_type=cerebellum, dev_stage=0 day neonate,
sex=mixed), (tissue_type=hippocampus, dev_stage=adult,
sex=male), (tissue_type=whole body, dev_stage=9 days
embryo, sex=mixed), (tissue_type=lung, dev_stage=13 days
embryo, sex=mixed), (tissue_type=lung, dev_stage=13 days
a 8 c 9 78 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3412 GGACACCAGGAAAAAAAAAACATCTTCTGAGGAGAATGTGCGTGGCTCCTATAACTCA 3471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 AGTAATAACTCCCATCAGCCCTTAACATCACGAGCCGAAGTGTGTCCCTGGGAGTTCGAG 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 CCCCTAGAACAACCAAATGCTGAAAGAAGCGTAACTTTACCTGCCTCCTCTGCTTTAAGT 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GGAGACCAGGAGAAACAGACATCTTCCTCTGTGGATATCATTCCTGGCTCCTGTAACTCA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCAAATAAGATAGCAGGGCCTAGGAAAGAAGAGATCTGGGATAGTTTTAAAGTGTA 3647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 170.4; DB 10; Length 356; Pred. No. 1.3e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BB255902 RIKEN full-length enriched, 7 days neonate musculus cDNA clone A730070K20 3', mRNA sequence. BB255902. GI:16398506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41;
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/dev_stage="16 days neonate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                  4.78;
82.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 82.6
Matches 195; Conservative
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GSS 14-MAY-2000

linear

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Submitted (12-APR-2000)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Caranthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.

1 (bases 1 to 632)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished

2 (bases 1 to 632)

2 (bases 1 to 632)

Sost-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                    Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : COAG151DG05LP1~end : T7"
9 others
                                                nigroviridis genome survey sequence T7 end of clone
library G from Tetraodon nigroviridis, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           370 GCGACCAGGCCGGCCAGCAGATCGTCCTGCAGGACCTGTCCAGCGTGGCCCGGCGGCTC 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          310 MACAACCGCACCGCCRACACGGGCTGGTACCACGACGCCAAGGAGGCCGAGAAGAAGCCC 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         400 AACTICCICAACGIGAIGCIGCAGAGCAAIAAGICGCGGGAGCAGAACTIGCAGGACGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCCACGCGCGAGGGCGCATCCTGCTCCAAGACCTGTCCTCCTCCGCACCCCGCACCTG
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Pred. No. 1.1e-29;
3; Mismatches 221; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="151N10"
                            DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_____/clone_lib="G"
/clone_lib="G"
/note="Genoscope sequence ID
                            632 bp
                                                                                                                                                                      GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
                                                                                                                                               GI:7864489
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AL205670.1
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Matches 334; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                   retraodon
151N10 of
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                                                                                                   sequence.
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                       LOCUS
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CNS02NOT/c
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JOURNAL
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KEYWORDS
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                                      sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y. Shibata,K., Itoh,M., Carninci,P., Sugahara,Computer-based methods for the mouse full-length cDnA encyclopedia: real-time sequence clustering for construction of a nonredundant cDnA library. Genome Res. 11 (2), 281-289 (2001)
Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anote—"Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was GAGAGAGAAGGATCCAAGAGCTTTTTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                      cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="RIKEN full-length enriched, 7 days neonate cerebellum"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1295 TCGTTAGCATGCTGGTGGTCTACCACTTTCGCAAAGCAAAGAGCATCCGGGCATCGGGCC 1354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 GGCCTCCCCGCAAAGAAGGCTGCCCCTTTTGTGNTGATGATTGTCCCATGCTTTTTTCTCAGG 183
                       RIKEN integrated sequence analysis (RISA) system--384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
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Pred. No. 3.8e-30;
0; Mismatches 38
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/dev_stage="7 days neonate"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/db_xref="taxon:10090"
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Best Local Similarity 83.4%;
Matches 191; Conservative
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases I to 358)

Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Tto, M., Kawai, J., Kojina, Y., Kondo, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numaski, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Shinata, K., Shinagawa, A., Shiraki, T., Sogabo, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akhira, S., Tanaka, T., Tomaru, T., Tayaki, Muramatsu, M. and Hayashizaki, Y., Riken Encyclopedia of Mouse Full-length CDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BB868702 RIKEN full-length enriched, pooled tissues, intestinal mucosa, etc. Mus musculus cDNA clone G630007J06 5', mRNA sequence. BB868702
                                                                                                        CGGGCCTGCCGGGGAAGTGGCCAGCCCTGGCCAGCGCGCACCCCTCCTTGCACCGGGCGC
                                                                                    TGGACACACTGACACACGCCACCACTTCCTCAACGTGATGCTGCAGAGCAATAAGTCGC
                                                                                                                                                                                                                                                         AGGGCGAGCCCAGCATCTCCCGGGCGGCCATCACCTTCAGCACCGATTCGCTGTCCGCAC
                                                                                                                                                                                                                                                                                    CGGCCCCACAGGTCTTCCTCCAGGCCACGCGCGAGGAGGCCGCATCCTGCTCCAAGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                    617 TGTCCTCCTCCGCACCCCACCTGGCCAACGCCACTCTGGAGACCGAGTGGTTCCACGGCC
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                                                                                                                                                                      GGGAGCAGAACTTGCAGGACGACGTGGATTGGTACCAGGCGCTGGTGTGGAGCCTTCTGG
                                                                                                                                                                                                                                                                                                                                                                                        650 GGACCGC---GGTGCTGCTCCAGGCGACCAGGCCGGCCAGCAGATCGTCCTGCAGGACC
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Teleostei; Euteleostei; Neoteleostei; Tetraodontidae; Tetraodon.

1 (bases 1 to 961)

1 (bases 1 to 961)

2 (bases 1 to 961)

Bernot, A., Fizames, C., Mincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
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//note="Genoscope sequence ID : C0AG227DG09LP1-end
/note="Genoscope sequence ID : C0AG227DG09LP1-end
1 276 c 353 g 157 t 2 others
                    250 RGCTTCCGGAAGAGGGTCCTGAGCCAGAACCCGAGCCTAGATTCTGTGGGCAGGGGGGAG
                                                                                                      760 GACGGGCTCGGCGGGACAAGAGCCACTTCAAGTGGTCTCCGCCTTATCTGGAGTGCGAG
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/db_xref="taxon:99883"
/clone="227N18"
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GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
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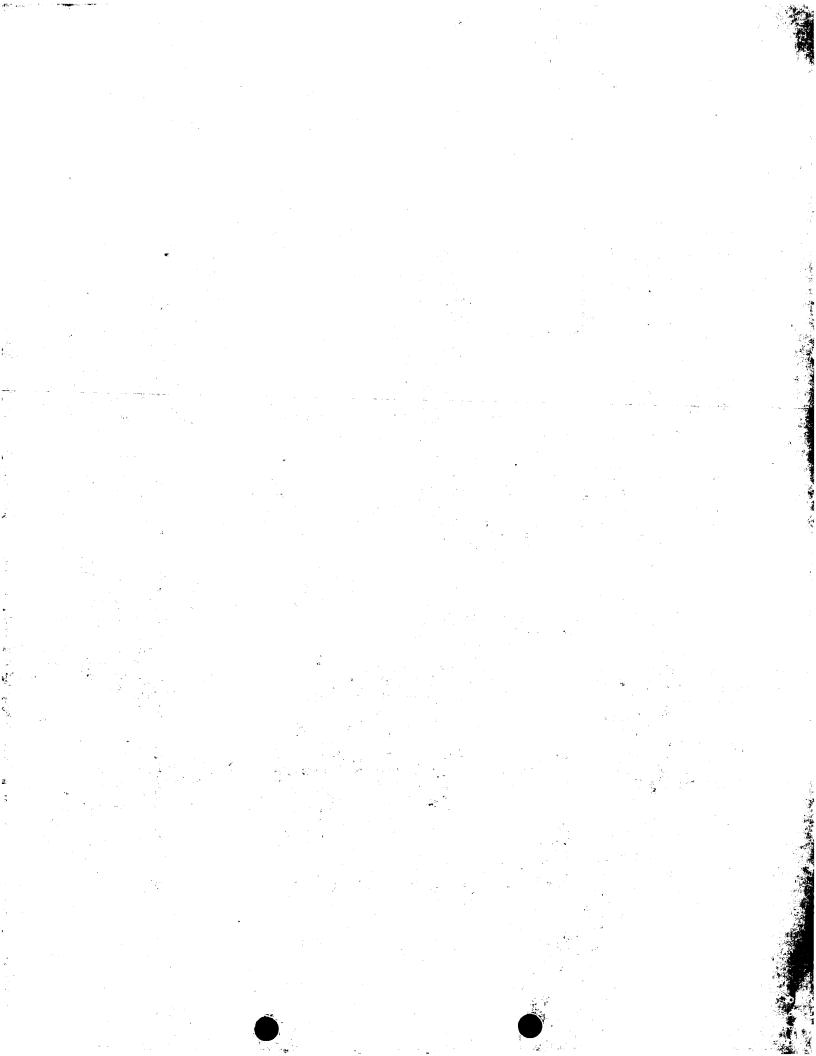
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// note="pooled tissues; (tissue_type=intestinal mucosa, dew_stage=adult, sex=male), (tissue_type=cossory axillary lymph node, dew_stage=adult, sex=male), (tissue_type=salult, sex=male), (tissue_type=spinal bladder, dew_stage=adult, sex=male), (tissue_type=spinal bladder, dew_stage=adult, sex=male), (tissue_type=spinal cord, dew_stage=11 days embryo), (tissue_type=spinal cord, dew_stage=11 days embryo), (tissue_type=brain, dew_stage=13 days embryo), (tissue_type=brain, dew_stage=13 days embryo), (tissue_type=brain, dew_stage=14 days embryo), (tissue_type=brain, dew_stage=16 days pregnant adult, sex=female), (tissue_type=cortex, dew_stage=0 day neonate), (tissue_type=corteb=lum, dew_stage=1 month neonate), (tissue_type=diencephalon, dew_stage=16 days neonate), (tissue_type=diencephalon, dew_stage=16 days neonate, sex=male), (tissue_type=medula oblongata, dew_stage=16 days neonate, sex=male), (tissue_type=medula oblongata, (tissue_type=cerebellum, dew_stage=8 days neonate, sex=male).

(tissue_type=testis, dew_stage=8 days neonate, sex=male)"
                                                                                                                                                                                                                                                                                      sequencing pipeline with 384 multicapillary sequencer. Genome Res. . 10 (11), 1757-1771 (2000) Kenno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
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7
URL:http://genome.gsc.riken.go.jp/.
Carlinci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
'M., Konno, H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                                                                                                       Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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/clone_lib="RIKEN full-length enriched, pooled tissues,
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                                                                                                                                                                                                                                                              RIKEN integrated sequence analysis (RISA) system -- 384 - format
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Pred. No. 3.1e-25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="C57BL/6"
/db_xref="taxon:10090"
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81.9%;
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Best Local Similarity
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High Throughput Sequencing Center
University of Mashington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3687
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 9072 row: M column: 7
Seg primer: SP6
Class: BAC ends
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AQ881884 152304_Al_GO4_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=9072 Col=7 Row=M, DNA sequence.
                                                                                                                                                                                                                                                                                                                                Mahairas,G.G., Waliace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 592)
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/sex="male"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99380589
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="Plate=9072 Col=7 Row=M"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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Location/Qualifiers
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                                                                                                                         AQ881884.1 GI:6313351
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TELEX: 899149,
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; IMMEDIATE SOURCE:
; CLONE: PTZ9Pt-F1s
US-08-232-463-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-232-463-14/c
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9728.320 Million cell updates/sec
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Sequence 35, 1
Sequence 7, Ap
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Sequence 30
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Sequence
Sequence
                                                                                                                             February 12, 2003, 22:48:02; Search time 115 Seconds
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-324-243-35
US-08-324-243-35
US-08-717-294-35
PCT-USS5-11511-35
US-08-073-384C-7
US-08-483-043-7
US-08-481-238-7
US-08-481-238-7
US-08-481-238-7
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US-08-481-238-7
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US-08-911-853-29
US-09-479-409-29
US-09-479-453-29
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1-08-756-386-7
1-08-823-516-7
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-08-758-314-7
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Maximum Match 100%
Listing first 45 summaries
                                                                                   nucleic search, using sw model
                                                                                                                                                                                                                                                                                                           IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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length: 2000000000
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  Sequence 1, As Sequence 3, As Sequence 1, As Sequence 1, As Sequence 1, As Sequence 22, Sequence 22, Sequence 23, As Sequence 
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Sequence 24,
Sequence 25,
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentur Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: DORRER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
ATTLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
US-09-141-027-1
US-08-972-008-3
US-08-972-008-1
US-09-267-409-1
US-09-479-1122-21
US-09-479-1122-22
US-09-479-1122-22
US-09-479-1122-24
US-09-479-1122-24
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US-08-479-1123-24
US-08-479-1123-24
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US-08-479-113-24
US-08-254-359A-2
US-08-471-066B-2
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APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 14, Application US/08232463 Patent No. 5670367
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APPLICATION NUMBER: EP 91 114
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (703)683-4109
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Length 7218;

DB 1;

1.7%; Score 62;

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TELEFAX:
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Best Local Similarity 7.3%; Pred. No. 2.7e-06;
Matches 32; Conservative 227; Mismatches 177; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/08232463 Patent No. 5670367 GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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ZIP: 22313-0299
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Patent No. 5786464
GENERAL INFORMATION:
APPLICANT: SEED, BRIAN
TITLE OF INVENTION: OVEREXPRESSION OF MAMMALIAN AND VIRAL
TITLE OF INVENTION: PROTEINS
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APPLICATION NUMBER: US/08/324,243
                                                                                                                                                                                                                                                         ch 1.3%; Score 48.4; DB 1;
1 Similarity 4.7%; Pred. No. 0.011;
19; Conservative 217; Mismatches 168;
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FILING DATE: 19-SEP-1994
ATTORNEY/ACENT INFORMATION:
NAME: CLARK, PAUL T
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/226001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                   INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy disk
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Best Local Similarity 4.7%;
(703)683-4109
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CORRESPONDENCE ADDRESS:
                                                                                                                                              TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZgpt-F1s
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CITY: Boston
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US-08-324-243-35
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWMARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
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22-SEP-1995
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225 Franklin Street
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FILING DATE: 22-SEP-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/324,243
FILING DATE: 19-SEP-1994
ATTORNEY/AGENT INFORMATION:
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Patent No. 5795737
TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 542-5070
                                            TELEX: 200154
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 2481 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                         1.3%;
                 (617) 542-50
(617) 542-8906
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Best Local Similarity 44.99
Matches 176; Conservative
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APPLICANT: SEED, BRIAN
APPLICANT: HAAS, JURGEN
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                                                                                                                  TYPE: nucleic STRANDEDNESS: TOPOLOGY: line
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CITY: Boston
STATE: Massach
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                               TELEFAX:
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1916 CGAGCCTGTGGAACTGGTTCGACATCACCAACTGGCTGTGGTACATCAAAAATCTTCATCA 1975
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Pred. No. 0.022;
0; Mismatches 216;
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Patent No. 6114148
GENERAL INFORMATION:
APPLICANT: SEED, BRIAN
APPLICANT: HAAS, JURGEN
TITLE OF INVENTION: HIGH LEVEL EXPRESSION OF
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
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SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/717,294
FILING DATE: 20-SEP-1996
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                     35,238
ER: 00786/294001
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176 Federal Street
                                                                                                 TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 2481 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
                        REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
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LECH, KAREN F.
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ZIP: 02110
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US-08-532-390-35
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US-08-717-294-35
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Matches 176;
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SOFTWARE: Patentin Release #1.0, Version #1.30B
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PCT-US95-11511-35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     599 GCATCCTGCTCCAAGACCTGTCCTCCTCCGCACCCCACCTGGCCAACGCCACTCTGGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                       o;
                                                                                                                                                                                                                                                                                                                                                                1.3%; Score 46.4; DB 3; Length 2481; 44.9%; Pred. No. 0.022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: OVEREXPRESSION OF MAMMALIAN AND VIRAL TITLE OF INVENTION: PROTEINS NUMBER OF SEQUENCES: 37 CORRESPONDENCE ADDRESS: ADDRESSE: Fish & Richardson STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches 216;
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                                                                                                    35,238
ER: 00786/345001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 35, Application PC/TUS9511511
GENERAL INFORMATION:
APPLICANT: SEED, BRIAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 0076
TELEPHONE: 617-428-0200
TELEPAX: 617-428-0200
                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 35:
                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 2481 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                     Matches 176; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Boston
STATE: Massachusetts
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
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PCT-US95-11511-35
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1976 TGATTGTGGGCGCCCTGGTGGGCCTCCGCATCGTGTTCGCCGTGCTGAGCATCGTGAACC 2035
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Pred. No. 0.022;
0; Mismatches 216; Indels
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APPLICANT: Dahlberg, James E.
APPLICANT: Dahlberg, James E.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Brow, Mary Ann D.
TITLE OF INVENTION: SYNTHESIS-DEFICIENT THERMOSTABLE DNA
TITLE OF INVENTION: POLYMERASE
NUMBER OF ENQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2156 GGCTCGTGCACGGCTTCCTGGCGATCATCTGG 2187
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                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, PAUL T
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/226001
TELECOMMUNICATION INFORMATION:
                         APPLICATION NUMBER: PCT/US95/11511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        California
: United States of America
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                                                                                                                                                                                                                                     TELERAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 2481 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                  (617) 542-5070
(617) 542-8906
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MEDIUM TYPE: Floppy disk
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Best Local Similarity 44.94
Matches 176; Conservative
CURRENT APPLICATION DATA
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SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          473 AGGCGCTGGTGGAGCCTTCTGGAGGGCGAGCCCAGCATCTCCCGGGCGGCCATCACCT 532
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Patent No. 5614402

GENERAL INFORMATION:
APPLICANT: DAHLBERG, JAMES E.
APPLICANT: BARICHEV, VICTOR I.
TAPLICANT: BAND, MARY ANN D.
TITLE OF INVENTION: DNA POLYMERASE
NUMBER OF SEQUENCES: 40

CORRESPONDENCES: 40

CORRESPONDENCES: HAVERSTOCK, MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 44.8; DB 1; Length 2502;
Pred. No. 0.06;
0; Mismatches 197; Indels 3
ourTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/073,384C
FILING DATE: 04-JUN-1993
CLASSIFICATION: 536
PROFT PAPLICATION: APPLICATION TO SAPERT APPLICATION TO SAPERT APPLICATION TO SAPERT APPLICATION TO APPLICATION TO SAPERT APPLICATION
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                                                                                                                                                                                                                                                                               CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/986,330
FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Carroll, Peter G.
REGISTRATION NUMBER: 32,837
REFERENCE/POCKET NUMBER: FORS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/795-8338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 2502 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2177 GCCGCCGCCTACGT 2192
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Matches 176; Conservative
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US-08-073-384C-7
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1820 TGGTGGCCCTGGACTATAGCCAGATAGAGCTCCGGGTCCTGGCCCACCTCTCCGGGGACG 1879
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                593 AGAGCCGCATCCTGCTCCAAGACCTGTCCTCCGCACCCCACCTGGCCAACGCCACTC 652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              413 TGATGCTGCAGAGCAATAAGTCGCGGGAGCAGAACTTGCAGGACGACCTGGATTGGTACC 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    533 TCAGCACCGATTCGCTGTCCGCACCGGCCCCACAGGTCTTCCTCCAGGCCACGCGCGAGG
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Pred. No. 0.06;
0; Mismatches 197; Indels
                                                                                                                                                           PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,384
FILING DATE: 06-UNN-1993
PRIOR APPLICATION NUMBER: US 07/986,330
FILING DATE: 07-DEC-1992
FILING DATE: 07-DEC-1992
ATTORNEY,AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FORS-01000
                                                                                                                                                                                                            US/08/254,359A
CALIFORNIA: UNITED STATES OF AMERICA
                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5691142
GENERAL INFORMATION:
APPLICANT: Dahlberg, James E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: FC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (415) 705-8410]
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 1.2%;
Best Local Similarity 46.8%;
Matches 176; Conservative (
                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 2502 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: CARROLL, PETER G. REGISTRATION NUMBER: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCGCCGCCTACGT 2192
                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
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                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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Pred. No. 0.06;
0; Mismatches 197; Indels 3
                APPLICANT: Brow, Mary Ann D.
TITLE OF INVENTION: SYNTHESIS-DEFICIENT THERMOSTABLE DNA
TITLE OF INVENTION: POLYMERASE
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                   ADDRESSEE: HAVERSTOCK, MEDLEN & CARROLL STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,384
FILING DATE: 04-JUN-1993
APPLICATION NUMBER: US 07/986,330
FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FORS-00613
                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/483,043 FILING DATE: 06-JUN-1995
                                                                                                                                                                                                  United States of America
                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Lyamichev, Victor I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: FO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/705-8410
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LENGTH: 2502 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 46.8
Matches 176; Conservative
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                                                                                                                                                             San Francisco
                                                                                                                                                                                California
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APPLICANT:
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STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAGCACCGATTCGCTGTCCGCACCGGCCCCACAGGTCTTCCTCCAGGCCACGCCGCGAGG 592
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                                                                                                                                                 APPLICANT: DAHLBERG, JAMES E.
APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: LYAMICHEV, VICTOR I.
TITLE OF INVENTION: SYNTHESIS-DEFICIENT THERMOSTABLE DNA
TITLE OF INVENTION: POLYMERASE
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
STREY: SAN FRANCISCO
STATE: CALIPORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.2%; Score 44.8; DB 46.8%; Pred. No. 0.06;
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                              Sequence 7, Application US/08481238 Patent No. 5795763 GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: FC TELECOMMUNICATION INFORMATION:
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TELEFAX: (415) 397-8338
INFORMATION FOR SEO ID NO: 7:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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Matches 176; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
US-08-481-238-7
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                                                                                                                                                                        2057 CCTACGAGGAGGCGGTGGCCTTCATTGAGCGCTACTTCCAGAGCTTCCCCAAGGTGCGGG 2116
                                                                                                         653 TGGAGACCGAGTGGTTCCACGGCCTCCGGCGCAAGTGGAGGCCCCACTTACACCGCGCG
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: DAHLBERG, JAMES E.
APPLICANT: LYAMICHEV, VICTOR I.
APPLICANT: BROW, MARY ANN D.
APPLICANT: OLDENBURG, MARY C.
APPLICANT: HEISLER, LAURA
TITLE OF INVENTION: DETECTION OF P53 MUTATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3: HAVERSTOCK, MEDLEN & CARROLL 220 MONTGOMERY STREET, SUITE 2200
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FILING DATE: 09-NOV-1994
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/254,359
FILING DATE: 06-UN-1994
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/073,384
FILING DATE: 04-UN-193
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/986,330
ATTORNEY, AGENT INFORMATION: NAME: CARRPOLL 1, PETER G. NAME: CAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FORS-01801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UNITED STATES OF AMERICA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-484-956-7; Sequence 7, Application US/08484956; Patent No. 5843654
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TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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TYPE: nucleic acid
STRANDEDNESS: single
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
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ZIP: 94104
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                                                                                                                                                                                                                                                                                               APPLICANT: Dahlberg, James E.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Brow, Mary Ann D.
TITLE OF INVENTION: 5' Nucleases Derived From Thermostable
NUMBER OF SEQUENCES: 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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APPLICATION NUMBER: US/08/471,066B
FILING DATE: 06-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSEE: Medlen & Carroll, LLP
1: 220 Montgomery Street, Suite 2200
San Francisco
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PRIOR APPLICATION BATA:
APPLICATION NUMBER: US 08/254,359
FILING DATE: 06-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/073,384
FILING DATE: 04-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/986,330
FILING DATE: 07-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, DIAINE E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-01800
TELEPHONE: (415,705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FORS-01800
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: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                             Sequence 7, Application US/08471066B Patent No. 5837450
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TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
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nucleic acid
EDNESS: single
2177 GCCGCCGCCTACGT 2192
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Matches 176; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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COUNTRY: UN
ZIP: 94104
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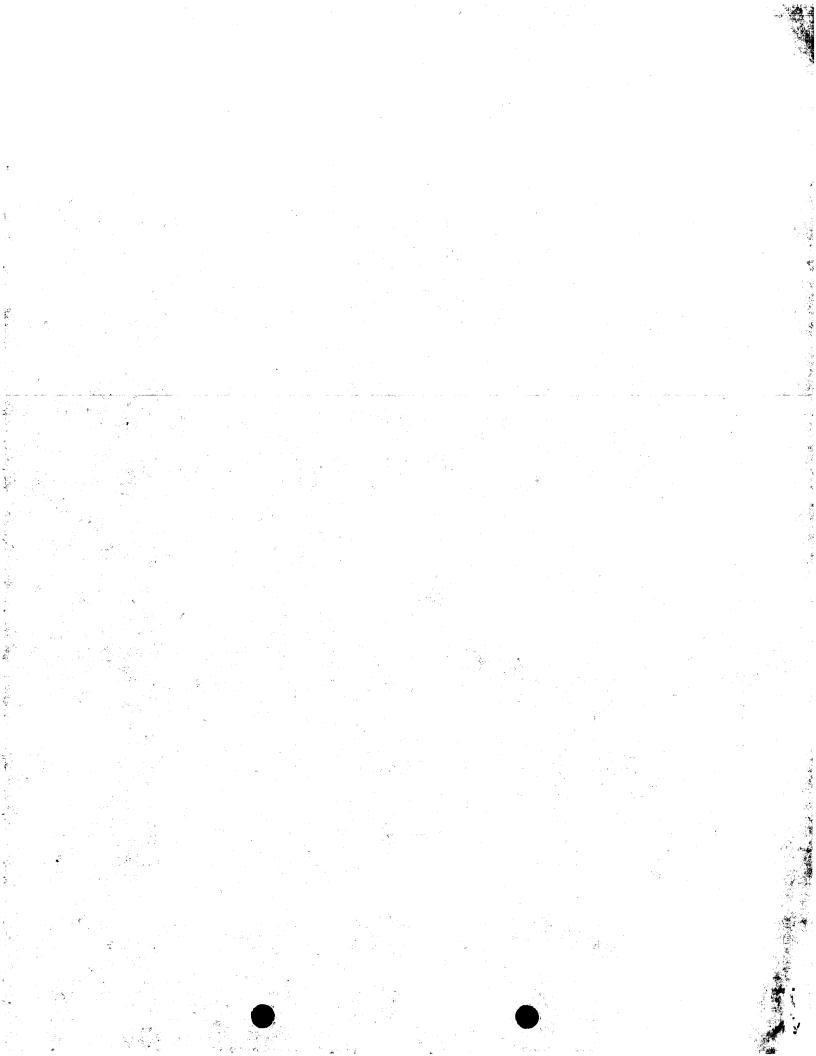
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94104
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                                                          US-08-757-653-7
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US-08-599-491-7
                                                                                                 Query Match
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                                                                                                               413 TGATGCTGCAGAGCAATAAGTCGCGGGAGCAGAACTTGCAGGACGACCTGGATTGGTACC 472
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                                                                              Gaps
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                                                                            3,
                                         Length 2502;
                                                                            Indels
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Patent No. 5843669
GENERAL INFORMATION:
APPLICANT: Raiser, Michael W. APPLICANT: Lyamichev, Victor I. APPLICANT: Lyamichev, Victor I. APPLICANT: Lyamichev, Natasha TITLE OF INVENTION: Cleavage Of Nucleic Acid Using TITLE OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
                                     1.2%; Score 44.8; DB 2; I
46.8%; Pred. No. 0.06;
tive 0; Mismatches 197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco STATE: California
COUNTRY: United "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FORS-02565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2502 base pairs
TYPE: nucleic acid
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TELECOMMUNICATION INFORMATION:
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                                                                          Conservative
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CLASSIFICATION: 435
                                     Query Match
Best Local Similarity
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                                                                          Matches 176;
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US-08-757-653-7
US-08-484-956-7
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                                                                                                                                                                  Gaps
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                                                                                                               Length 2502;
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Patent No. 5846717
GENERAL INFORMATION:
APPLICANT: GROTELUESCHEN HALL, JEFF S.
APPLICANT: LYAMICHEV, VICTOR
APPLICANT: OLIVE, DAVID M.
APPLICANT: PRUDENT, JAMES R.
TITLE OF INVENTION: DETECTION OF NUCLEIC ACID SEQUENCES BY
                                                                                                                                                                  Indels
                                                                                                         1.2%; Score 44.8; DB 2; illarity 46.8%; Pred. No. 0.06; Conservative 0; Mismatches 197;
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STREET: 220 MONTGOMERY STREET, SUITE 2200
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APPLICATION NUMBER: US/08/599,491
FILING DATE: 23-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: INGOLIA, DIANE E.
REJISTRATION UNDBER: P-40,027
REFERENCE/DOCKET NUMBER: FORS-
TELECOMMUNICATION INFORMATION:
TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
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CORRESPONDENCE ADDRESS:
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Matches 176; Conserva
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Patent No. 598557
GENERAL INFORMATION:
APPLICANT: Prudent, James R.
APPLICANT: Lyamichev, Victor I.
TITLE OF INVENTION: Invasive Cleavge Of Nucleic Acids NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                              Query Match 1.2%; Score 44.8; DB 2; 1
Best Local Similarity 46.8%; Pred. No. 0.06;
Matches 176; Conservative 0; Mismatches 197;
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220 Montgomery Street, Suite 2200
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STATE: California
COUNTRY: United States Of America
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FILING DATE: 12-JUL-1996
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2502 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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PRIOR APPLICATION DATA:
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Best Local Similarity 46.8%; Pred. No. 0.06;
Matches 176; Conservative 0; Mismatches 197;
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                                                                                                                                        FORS-02564
     US 08/599,491
                                                                                                                             REFERENCE DOCKET NUMBER: FOR TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410 TELEFAX: (415) 397-8338 INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERISTICS: LENGTH: 2502 base pairs
                                                                           NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic) US-08-756-386-7
                              FILING DATE: 24-JAN-1996
ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: single
APPLİCATION NUMBER:
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Query Match 100.0%; Score 3648; Best Local Similarity 100.0%; Pred. No. 0; Matches 3648; Conservative 0; Mismatches
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Sequence 5, Appli
Sequence 3, Appli
Sequence 82, Appli
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11759.574 Million cell updates/sec
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/cgn2_6/ptodata/1/pubna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/USO6_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-476-242-8
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US-09-764-898-82

US-09-799-183-4

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Maximum Match 100%
Listing first 45 summaries
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TGGAGCCGCTCCACCGATGGCACCATCTTGGCGCAGAAACTCGCCGAGGAGGTGCCCATG

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Sequence 6, Appli Sequence 26, Appli Sequence 16, Appli Sequence 17, Appli Sequence 17, Appli Sequence 13, Appli Sequence 13, Appli Sequence 10, Appli Sequence 11, Appli Sequence 17, Appli Sequence 7, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 50, Appli Sequence 50, Appli Sequence 50, Appli Sequence 40, Appl Sequence 3, Appli Sequence 483, App APPLICANT: Hilbun, Erin TITLE OF INVENTION: NO. US20020038013A1el Human Membrane Proteins and TITLE OF INVENTION: No. US20020038013A1el Human Membrane Proteins and TITLE OF INVENTION: Polynucleotides Encoding the Same File Reference: LEX.0129-USA CURRENT APPLICATION NUMBER: US/09/775,181
PRIOR APPLICATION NUMBER: US 60/180,414
PRIOR FILING DATE: 2000-02-04 US-09-476-242-6 US-09-476-242-26 US-09-476-242-26 US-09-476-242-16 US-09-476-242-17 US-09-476-242-17 US-09-476-242-17 US-09-476-242-13 US-09-476-242-13 US-09-476-242-13 US-09-476-242-13 US-09-476-242-10 US-09-476-242-11 US-09-476-242-12 US-09-476-242-12 US-10-033-297-7 US-10-033-297-7 US-10-013-329-7 US-10-013-329-12 US-10-101-392-1 US-10-023-529-45 US-09-976-740-50 2 US-10-023-529-50 2 US-10-023-523-50 US-10-066-500-40 US-10-053-107-3 US-10-028-072-483 NUMBER OF SEQ ID NOS: 5 SOFTWARE: FastSEQ for Windows Version 4.0 Sequence 1, Application US/09775181 Patent No. US20020003013A1 GENERAL INFORMATION: APPLICANT: Donoho, Gregory 12425 12425 12425 12425 2498 2498 Homo sapiens LENGTH: 3648 RESULT 1 US-09-775-181-1 ; ORGANISM: Ho US-09-775-181-1 TYPE: DNA SEQ ID NO 1 42. 42. 

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Sequence 5, Application US/09775181
Sequence 10. US/09020038013A1
GENERAL INFORMATION:
APPLICANT: Donoho, Gregory
APPLICANT: Hilbun, Erin
TITLE OF INVENTION: No. US/20020038013A1e1 Huma; TITLE OF INVENTION: Polynucleotides Encoding
FILE REFERENCE: LEX-0129-USA 0; Mismatches Score 3525; Pred. No. 0; CURRENT APPLICATION NUMBER: US/09/775,181
CURRENT FILING DATE: 2010-02-01
PRIOR APPLICATION NUMBER: US 60/180,414
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5

1753 2288 1807 2347 2407 ||||| |GTTGGTATGTGGTCACTTGTTTCGTATGATGGTCTTACCATTTTTCAGTAG 2228 1753 1867 1927 2468 1987 2528 2047 2588 2107 2648 2167 2708 2227 2287 2888 2948 3008 3068 ACATCCGATCACCTCATCTTCAATATGTGCCTCATTGACCGCTGGGACTAC 1740 2467 2527 TGGACTTCATCTGTGCCCAGAATTTGGAGAAACAGATTTCACTTATTGGC 2108 GCCGGCAGTGCTCTAAAGAGGACAAGGAGGCGCCGACCATGGCACAGCCA TATTCCATACAATTAGATTTGTTCTTGCCTCAAGACTTCAGTCTGATTGGA TGTATTTTGCACATACTCATTTGACTGTGACAGTCACCATTGGGTTGCTTT AGTITICACATICAAGCAATAACCCACGAGATGATATIGCTACAGAAGCAT AGCTAGACATGGGCCGATCTGGATCCTACCTGAACAGCAGTATCAATTCAG AGCACAGCTTGGATCCAGAGGACATTCGGGACGAGCTGAAAAAACTCTATG AGCACAGCTTGGATCCAGAGGACATTCGGGACGAGCTGAAAAACTCTATG CGAAGAAGGGCCTAGGTCGTTCCATGAGACGCATTACGGAGATCCCAG GCCGGCAGTGCTCTAAAGAGGACAAGGAGGGCGCCCGACCATGGCACAGCCA CCCTGAAAAACCGAGTCTTCTCACTCAAGAAATCCCACAGGCACTTATGACC AGCCTGAGTCCACGGAGTCGGTGCCGTTGGTGTGCAAGTCAGCAAGCGCTC CATTCCATGAGCCCCGCTATATGGCTGTTGCAGTTCACAATGAGCTCATCA CCCTCATCAGGAAGAACCCCCCAGAGTCTTCAGGGAACACAGGGAAATCCA TGACTTCTTTAAAAGTCTTGCCAGACTCTTTAGTAAAGCCTAAACTAATCT 'GTTG-----

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       APPLICANT: DOORDOOD, Gregory
APPLICANT: Hilbun, Erin
ATTLE OF INVENTION: No. US20020038013A1e1 Human Membrane Proteins
TITLE OF INVENTION: Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0129-USA
CURRENT APPLICATION NUMBER: US/09/775,181
CURRENT APPLICATION NUMBER: US 60/180,414
PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                     Length 1800;
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                                                                                                                                                                                                     DB 10;
                                                                                                                                                                                                                            16;
                                                                                                                                                                                                    Score 1756.4;
Pred. No. 0;
0; Mismatches
                                                                                                            NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version
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                                                                                                                                                                                                     48.1%;
99.1%;
                                                                                                                                                                                                     Query Match 48.1
Best Local Similarity 99.1
Matches 1766; Conservative
                                                                                                                                                                  ; ORGANISM: Homo sapiens US-09-775-181-3
GENERAL INFORMATION
                                                                                                                                             LENGTH: 1800
                                                                                                                                                          TYPE: DNA
                                                                                                                                    SEQ ID NO 3
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Sequence 3, Application US/09775181

RESULT 3 US-09-775-181-3

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1676 GCCCGGCCCGAGCGTGCCCCCGGAGCGCCGACGTGTGCTGGAGCCCAGCGCGGAGAGGACG 1735
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                                                                                                                                                                                                                                                                                                                                                     Score 51.2; DB 10;
Pred. No. 0.00064;
0; Mismatches 158;
                                                       TITLE OF INVENTION: Nucleic Acids, Proteins, TITLE OF INVENTION: Nucleic Acids, Proteins, FILE REFERENCE: PJZ01 CURRENT APPLICATION NUMBER: US/09/764,898 Prior application data removed - consult PALM NUMBER OF SEQ ID NOS: 311 SOFTWARE: Patentin Ver. 2.0
Sequence 82, Application US/09764898
Patent No. US20020090673A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 4, Application US/09999183; Patent No. US20020147169A1; GENERAL INFORMATION:
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48.08;
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                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens US-09-764-898-82
                                                                                                                                                                                                                                                                                                                                                                             Similarity
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Matches 146;
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SEQ ID NO 82
LENGTH: 254
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  721 CAGGGGCCCCGGGGCCTGGGCCACAGCTGGCGGCGAAGGACGGGCTCGGCGGGGACAAG
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                                          AGCCACTTCAAGTGGTCTCCGCCTTATCTGGAGTGCGAGAACGGGAGTTACAAGCCCGGG
                                                                 TGGCTGGTTACTCTTTCCTCTGCCATCTACGGGTTGCAGCCTAACCTGGTCCCGGAATTC
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ö Gaps ó Length 2571; Indels Score 48; DB 10; L Pred. No. 0.0053; 0; Mismatches 215; ; OTHER INFORMATION: Codon optimised env sequence US-09-999-183-4 APPLICANT: MITROPHANOUS, et al.
TITLE OF INVENTION: In Vivo Selection Method
FILE REFERENCE: 674523-2009
CURRENT APPLICATION NUMBER: US/09/999,183
CURRENT FILING DATE: 2001-11-29
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 1999-06-03
PRIOR FILING DATE: 1999-06-03
SOFTWARE: SEQUING
SEQUING: 26 ; Query Match 1.3 Best Local Similarity 45.2 Matches 177; Conservative ö

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US-09-799-462A-17
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Matches 134;
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                                         1883 CCTGGATGCAGTGGGAGCGCGGAGATCGATAACTACACCAGCCTGATCTACAGCCTGCTGG 1942
                                                                                                                                1943 AGAAGACCCAGACCCAGCAGGAGAACGAGCAGGAGCTGCTGGAGCTGGACAAGTGGG 2002
                                                                                                                                                                                                                        2003 CGAGCCTGTGGAACTGGTFCGACATCACCAACTGGCTGTGGTACATCAAAATCTTCATCA 2062
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CCTCCTTGCACCGGGCGCTGGACACACTGACACGCCACCAACTTCCTCAACGTGATGC 418
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                                                                                      419 TGCAGAGCAATAAGTCGCGGGAGCAGAACTTGCAGGACGACGTGGATTGGTACCAGGCGC
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TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF
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REFERENCE/DOCKET NUMBER: 24601-402G
TELECOMMUNICATION INFORMATION:
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FILING DATE: 10-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2243 GGCTCGTGCACGGCTTCCTGGCGATCATCTGG 2274
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ADDRESSEE: Heller Ehrman White
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FILING DATE: 07-AUG-1996
APPLICATION NUMBER: 08/682,080
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FILING DATE: 10-APR-1996
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OPERATING SYSTEM: DOS
SOFTWARE: FASISEQ VERSION 1.5
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17, Application US/09799462A Patent No. US20020160970A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 15-JUL-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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COMPUTER READABLE FORM:
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2561 GTAAAAAACTAACACAAAAACTAAAAGAAGACAGCGAGGCTGAGTCCACGGAGTCGGTGC 2620
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                                                                                                                                                                                                                                                                                                                                                  1.3%; Score 47; DB 9; Length 42999;
48.0%; Pred. No. 0.081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Heller Ehrman White & McAuliffe LLP STREET: 4350 La Jolla Village Drive, 7th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40277 AAGAAACAAAAGAAAGAAAGAAAAGAAAAGAAAAAGAAAA 40239
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TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES,
                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/125,767
FILING DATE: 17-Apr-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 09/724,693
FILING DATE: 28-NOV-2000
FILING DATE: 10-APR-1997
FILING DATE: 10-APR-1997
APPLICATION NUMBER: 08/695,191
FILING DATE: 07-ANG-1996
APPLICATION NUMBER: 08/682,080
FILING DATE: 15-JUL-1996
                                                                                                                                                                                                                     FRAGMENT TYPE: <Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
                  ENCE CHARACTERISTICS:
LENGTH: 42999 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Patent No. US20020160410A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METHODS
                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: Genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette
INFORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 92122
                                                                                                                                                                         HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                            Similarity
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1.3%;
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                                  Matches 100; Conservative
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Matches 192; Conservative
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                                                                                                                                                                                                                                                                                                              542 CACAGCGGCC 551
Query Match
Best Local Similarity
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LENGTH: 2298
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US-09-476-242-22
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APPLICANT: Olga Bandman
TITLE OF EINVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
SOFTWARE: PERL PROGRAM
SEQ ID NO 309
LENGTH: 2724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.3%; Score 47; DB 9; Length 42999; Best Local Similarity 48.0%; Pred. No. 0.081; Matches 134; Conservative 0; Mismatches 145; Indels
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                                              NAME: Seidman, Stephanie L
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24601-402J
TELECOMMUTCATION INFORMATION:
TELEPHONE: 858-450-8403
TELEFRONE: 858-587-5360
                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-125-767-17
APPLICATION NUMBER: 08/629,822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COTHER INFORMATION: a, t, c, g, or other US-10-044-090-309
                                                                                                                                                    TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 42999 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
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; Sequence 309, Application US/10044090
; Patent No. US20020137081A1
                FILING DATE: 10-APR-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                              <Unknown>
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OTHER INFORMATION: Incyte
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                                                                                                                            547 CTGTCCGCACCGGCCCCACAGGTCTTCCTCCAGGCCACGCGCGGAGGAGAGCCGCATCCTG 606
                                                                                                                                                               359 CCTCCTTGCACCGGGCGCTGGACACACTGACACGCCACCAACTTCCTCAACGTGATGC 418
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                                                               Gaps
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                                                                                                                                                                                                                                                                                     GCATCCTGCTCCAAGACCTGTCCTCCGCACCCCACCTGGCCAACGCCACTCTGGAGA
                                                                                                                                                                                                                                                     607 CTCCAAGACCTGTCCTCCTCCGCACCCCACCTGGCCAACGCCACTCTGGAGACCGAGTGG
                                                                                                                                                                                                                                                                                                                                                                           667 ITCCACGGCCTCCGGCGCAAGTGGAGGCCCCCACTTACACCGCCGCGCGCCCCAATCAGGGG
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Score 46; DB 12; Length 2724;
Pred. No. 0.021;
                                                               Indels
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Patent No. US20020146683A1
GENERAL INFORMATION:
APPLICANT: BARNETT, Susan
APPLICANT: HARTOG, Karin
APPLICANT: HARTOG, Karin
TITLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES
FILE REFERENCE: 1605.002
CURRENT APPLICATION NUMBER: US/09/476,242
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN VET. 2.0
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44.0%; Pred. No. 0.024;
tive 0; Mismatches 244;
                                                               90;
                                                                  0; Mismatches
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                                                                                                                                                                          SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 24
LENGTH: 2298
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Best Local Similarity 44.09
Matches 192; Conservative
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  APPLICANT: BARNETT, Susan
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US-09-476-242-3
                                                                                                                                                                                                                                               TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             359 CCTCCTTGCACCGGGCGCTGGACACACTGACACGCCCACCAACTTCCTCAACGTGATGC 418
1961 CCCTGGTGCACGCCCTGCTGCACCTGGGACGACCTGCCGCACCTGTGCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  419 TGCAGAGCAATAAGTCGCGGGAGCAGAACTTGCAGGACGACGTGGATTGGTACCAGGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCATCCTGCTCCAAGACCTGTCCTCCGCACCCCACCTGGCCAACGCCACTCTGGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          479 TGGTGTGGAGCCTTCTGGAGGGCGAGCCCAGCATCTCCCGGGCGGCGCCATCACCATCAGCA
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                                                                                                                                                                              Sequence 23, Application US/09476242

Fatent No. US20020146683A1

GENEBAL INNORMATION:

APPLICANT: BARNETT, Susan

APPLICANT: HARTOG, Karin

APPLICANT: MARTON, Eric

TILLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES

FILE REPERENCE: 1605.002

CURRENT APPLICATION NUMBER: US/09/476,242

CURRENT FILING DATE: 1999-12-30

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 1.2%; Score 45.6; DB 10;
Local Similarity 44.0%; Pred. No. 0.024;
les 192; Conservative 0; Mismatches 244;
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US-09-476-242-24
; Sequence 24, Application US/09476242
; Patent No. US20020146683A1
; GENERAL INFORMATION:
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                                                                                         2021 GCTACCACCGCCTGCG 2036
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US-09-476-242-23
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LENGTH: 2298
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US-09-476-242-24
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Patent No. US20020146683A1

GERERAL INFORMATION:
APPLICANT: BARNETY, Susan
APPLICANT: HARTOG, Karin
APPLICANT: MARTIN, EDILETIE HIV ENV POLYPEPTIDES
TITLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES
CURRENT APPLICATION WOMBER: US/09/476,242
CURRENT APPLICATION WOMBER: US/09/476,242

CURRENT APPLICATION PORTS: 1999-12-30

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn Ver. 2.0

SOFTWARE: 2310
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45.6; DB 10;
Pred. No. 0.024;
0; Mismatches 244;
APPLICANT: HARTOG, Karin
APPLICANT: MARTIN, ELIC
TITLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES
FILE REFERENCE: 1605.002
CURRENT APPLICATION NUMBER: US/09/476,242
CURRENT FILING DATE: 199-12-30
NUMBER OF SEQ ID NOS: 26
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TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity
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. OTHER INFORMATION: Asn425-Lys432
US-09-476-242-21
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Vall20-Ala204
US-09-476-242-3
                                                                                                                                                                                                                                                                                             479 TGGTGTGGAGCCTTCTGGAGGGGGAGCCCAGCATCTCCCGGGCGGCGATCACCTTCAGCA
                                                                                                                                                                                                                                                                                                                                 CCAGCCTGTGGAACTGGTTCGACATCAGCAAGTGGCTGTGGTACATCAAGATCTTCATCA
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Patent No. US20020146683A1

GENERAL INFORMATION:
APPLICANT: HARTOG, Karin
APPLICANT: HARTOG, Karin
APPLICANT: HARTN, Elic
TILLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES
FILE REFERENCE: 1605.002

CURRENT APPLICATION NUMBER: US/09/476,242

CURRENT FILING DATE: 1999-12-30

NUMBER OF SEO ID NOS: 26

SOFTWARE: Patentin Ver. 2.0
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                                                                    Score 45.6; DB 10;
Pred. No. 0.024;
0; Mismatches 244;
                                                                      Query Match 1.2%;
Best Local Similarity 44.0%;
Matches 192; Conservative
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LENGTH: 2310
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US-09-476-242-4
1793 TGATCGTGGGGGCCTGGTGGGCCTGCGCATCGTGTTCACCGTGCTGAGCATCGTGAACC
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                                                                                                479 IGGIGIGGAGCCTICTGGAGGCCGAGCCCAGCATCTCCCGGGCGGCCATCACCTTCAGCA
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Sequence 4, Application US/09476242

Sequence 4, Application US/09476242

Patent No. US20020146683A1

GENERAL INFORMATION:
APPLICANT: BARNETY, Susan
APPLICANT: HARTON, Eric
TITLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES
FILE REFERENCE: 1605.002

CURRENT APPLICATION UNDBER: US/09/476,242

CURRENT FILING DATE: 1999-12-30

NUMBER OF SEQ ID NOS: 26

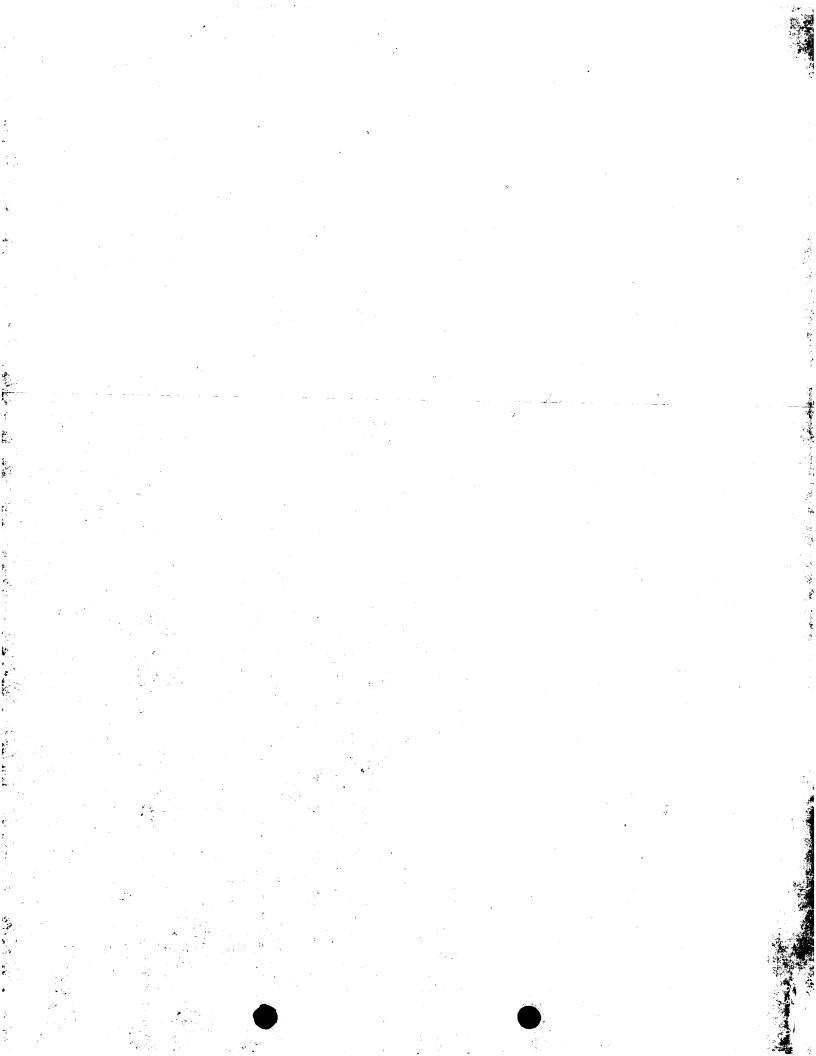
SOFTWARE: PatentIn Ver. 2.0
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Pred. No. 0.024;
0; Mismatches 244;
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                         1979 CCCTGGTGCACGCCCTGCTGCTCGGACGACGTGCGCAGCCTGTGCTTTCA 2038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Description of Artificial Sequence: Vall20-Thr202 US-09-476-242-8
659 CCGAGTGGTTCCACGGCCTCCGGCGCAAGTGGAGGCCCCACTTACACGCGCCGGGCCCCA
                                                                             719 ATCAGGGGCCCCGGGGCCTGGGCCACAGCTGCCGGCGCAGAGGACGGGCTCGCGGGGACA
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                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/09476242;
Fatent No. US20020146683A1
GENERAL INFORMATION:
APPLICANT: HARTOG, Karin
APPLICANT: MARTIN, Eric
TITLE OF INVENTION: MODIFIED HIV ENV POLYPEPTIDES
FILE REFERENCE: 1605.002
CURRENT APPLICATION NUMBER: US/09/476,242
CURRENT FILING DATE: 1999-12-30
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
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Search completed: February 13, 2003, 00:16:20 Job time : 246 secs



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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
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February 15, 2003, 04:23:28 - protein search, using sw model OM protein Run on:

; Search time 62.2905 Seconds (without alignments) 2599.103 Million cell updates/sec

Perfect score:

US-09-775-181-2 6382 1 MGAMAYPLLCLLLAQLGLG......LSANKIAGPRKEEIWDSFKV 1215 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

908470 segs, 133250620 residues Searched:

908470

tal number of hits satisfying chosen parameters: seq length: 0 seq length: 2000000000 imum DB: Maximum DB:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		Description	Human G-protein co	Human G-protein co	Drosophila melanog	Drosophila G-prote	Drosophila melanog	Drosophila melanog	Drosophila melanog	Drosophila G-prote	D. melanogaster GA	Drosophila melanog
		ID	AAE06642	AAE06643	ABB70858	AAU38983	ABB69976	ABB67184	ABB62615	AAU38942	AAB86160	ABB67185
		DB	22	22	22	22	22	22	22	22	22	22
		Match Length DB ID	1215	599	699	699	1677	264	1221	1221	1220	176
æ	Query	Match	100.0	48.9	9.0	9.0	4.8	4.4	4.0	4.0	3.8	3.7
		Score	6382	3119.5	571.5	571.5	307	281	254	254	243.5	238.5
	Result	No.	П	7	m	4	5	9	7	α	6	10

		Drosophila G-prote	Ω	Amino acid sequenc	Mouse metabotropic	Rat metabotropic q	Drosophila melanog		Human metabotropic	Drosophila melanog	Human mGluR5a. Ho	pmGluR2/CaR*Galpha	Human pmGluR2-CaR*	Human metabotropic	hmGluR5b. Homo sa	Human metabotropic	Human ph2SPMGluR3-	Chimeric receptor	Human mGluR5b. Ho	pmGluR2/CaR*Galpha	Human pmGluR2-CaR*	HSmGluR1. Homo sa	Human phmGluR4-CaR	Drosophila melanog	Amino acid sequenc	Human polypeptide	Peptide #2376 enco	Peptide #2403 enco	Protein #2313 enco	Human brain expres	Human bone marrow	Peptide #2327 enco	Human peptide enco	Lactococcus lactis
AAB86161	ABB59497	AAU38927	AAR25080	AAW25763	AAY28562	AAY28563	ABB60327	ABB58769	AAE01156	ABB58022	AAR64253	AAY49134	AA015100	AAY28564	AAB47220	AAE01157	AA015105	AAB47219	AAR64254	AAY49129	AA015095	AAR42199	AA015102	ABB69279	AAW25765	AAM40114	ABB29725	ABB34897	ABB20314	AAM55707	AAM68085	64	ABG37612	ABB54963
22	22	22	13	18	20	20	22	22	22	22	16	20	23	20	22	22	23	22	16	20	23	14	23	22	18	22	22	22	22	22	22	22	23	23
1305	1305	1305	1199	1219	19	17	3111	18	18	1812	18	39	39	21	21	1212	1402	04	21	39	1394	19	1422	48	05	19	1325	32	1325	32	1325	32	1325	1072
3.6	3.6	3.6	3.5	3.4	3.3	3.3	3.2	3.2	3.2	3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.1	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	3.0	5.9
232	227.5	227.5	223.5	220	212	210	205.5	205	204	198.5	198	198	198	97	197.5	97	97	194	93	193.5	93	193	193	193	190	Н	88	88	188.5	88.	188.5	88	88.	m
11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	38	40	41	42	43	44	45

## ALIGNMENTS

AAE06642 standard; Protein; 1215 AA 16-OCT-2001 (first entry) AAE06642; **AAE**06642 

Human G-protein coupled receptor (NGPCR) #1

Human; G-protein coupled receptor; NGPCR; gene therapy; cancer; diabetes; inflammation; immune disorder; heart disease; obesity; coronary disease; metabolic disorder; physiological disorder; therapeutic; drug screening; signal transduction; behavioural disorder.

Homo sapiens

WO200157086-A2.

09-AUG-2001

01-FEB-2001; 2001WO-US03648

04-FEB-2000; 2000US-0180414.

(LEXI-) LEXICON GENETICS INC.

Donoho G, Hilbun E;

WPI; 2001-488870/53. N-PSDB; AAD12292.

Novel isolated polynucleotides encoding human G protein coupled

20

Thu Feb

a

us-09-775-181-2.rag

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The present sequence is human G-protein coupled receptor (NGPCR) which is a 7 transmembrane protein of G-protein coupled receptor (GPCR) super family. NGPCR is expressed in hypothalamus, foctal brain, brain, cerebellum and testis. NGPCR spans the cellular membrane and is involved in signal transduction pathways. Human NGPCR is useful for treating obssity, inflammation, immune disorders, diabetes, heart and coronary disease, metabolic disorders and cancer. NGPCR's are also used as reagents in assays for screening compounds that are useful in the therapeutic treatment of physiological and behavioural disorders. NGPCR is useful for identifying compounds that meduate NGPCR gene expression and/or gene product activity. NGPCR DNA is also useful for the diagnostic and prognostic evaluation of disorders related to NGPCR function.

Nucleotide constructs encoding functional NGPCR and mutant NGPCR variants are used in gene therapy. NGPCR probes are also useful for the identification, selection and validation of novel molecular targets for
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tor (NGPCR), useful as probe and for treating disease involving detecting mutant NGPCR or abnormally expressed NGPCRs for
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Human, G-protein coupled receptor, NGPCR, gene therapy, cancer, diabetes, inflammation, immune disorder, heart disease, obesity, coronary disease, metabolic disorder, physiological disorder; therapeutic; drug screening;
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KSLSVIASAKEKTLGLAGKTQTAGVEERTKSQKPLPKDKETNRNHSNSDNTETKDPAPQN 960
                                                                                                                EETTENSTLESLSGKKLTQKLKEDSEAESTESVPLVCKSASAHNLSSEKKTGHPRTSMLQ
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                                                                                    LYAQLEIYKRKKMITNNPHLQKKRCSKKGLGRSIMRRITEIPETVSRQCSKEDKEGADHG
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N-PSDB; AAD12293.
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The present sequence is nummin of protein coupled receptor (GPCR) super family. NGPCR is expressed in hypothalamus, foetal brain, brain, cerebellum and testis. NGPCR spans the cellular membrane and is involved in signal transduction pathways. Human NGPCR is useful for treating cobesity, inflammation, immune disorders, diabetes, heart and coronary disease, metabolic disorders and cancer. NGPCR's are also used as concerning compounds that are useful in the charapeutic treatment of physiological and behavioural disorders. NGPCR is useful for identifying compounds that modulate NGPCR gene expression and/or gene product activity. NGPCR DNA is also useful for the diagnostic and/or gene product activity. NGPCR DNA is also useful for the diagnostic and prognostic evaluation of disorders related to NGPCR function.

C Nucleotide constructs encoding functional NGPCR and mutant NGPCR variants are used in gene therapy. NGPCR probes are also useful for the identification, selection and validation of novel molecular targets for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                                                    The present sequence is human G-protein coupled receptor (NGPCR) which
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Novel isolated polynucleotides encoding human G protein coupled receptor (NGPCR), useful as probe and for treating disease involving GPCR, detecting mutant NGPCR or abnormally expressed NGPCRs for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    22; Length 599;
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Pred. No. 1.3e-220;
2; Mismatches 2;
                                                                                  Claim 4; Page 70-71; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 98.5%;
Matches 585; Conservative
                                                   diagnosing disease
                                                                                                                                                                                                                                                                                                                                                                                                                599 AA;
                                                                                                                                                                                                                                                                                                                                                                                  drug discovery.
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 GKWPALASAHPSLHRALDTLTHATNFLNVMLQSNKSREQNLQDDLDWYQALVWSLLEGEP 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 SISRAAITFSTDSLSAPAPQVFLQATREESRILLQDLSSSAPHLA-----NATLETEWF 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HNKAYLGSYWRE------LGAAWNSTDGTQ-----EWGAPFRDCNLLTRRWL 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HG---LRRKWRPHLHRRGPNQGPRGLGHSWRRKDGLGGDKSHFKWSPPYLECENGSYKPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 338 MPIKGL-GFVLGAYECICKAGFYHPGVLPVNNFRRRGPDQHISGSTKDVSE--EAYVCLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 GKWPC-RMFYDYTDIAEDAARQFIEFL----SGKFPNANTPIAID-----EP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48 --TRAEVSRRANGIAS-----YALNEDDNLLAFAIAAPSIHTVVVKFRDNVTIPPDQV
                                                                                                                       Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 39366; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 669;
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                                                                                         Drosophila melanogaster polypeptide SEQ ID NO 39366
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ABB70858 standard; Protein; 669 AA.
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11-JUL-2000; 2000US-0614150.
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genes from Drosophila and
                                                                                                                                                                      Drosophila melanogaster
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                                                                                                                                                                                                 WO200171042-A2
                                                                                                                                      pharmaceutical
                                                           26-MAR-2002
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RESULT 3 ABB70858

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The invention relates to sixty six novel isolated Drosophila melanogaster G-protein coupled receptors (GPCR). The GPCR proteins and nucleic acids are useful in the treatment and diagnosis of GPCR-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila; G-protein coupled receptor; GCPR; insecticide; diagnostic;
                                                                                                                                                            626
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                                                                    298 ASGMWTVLETILLGIVLLYASVAVHFFPASTERCLLEPWLRELGFITCYGAIILKLYRHL 357
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                                                                                                                                                                                                                                                                                                                        CSKKGLGRSIMRRITEIPETVSRQCSKEDKEGADHGTAKG-----TALIRKNPPESSGN 798
                                                                                                                                                                                                                FHTIRFVLASRLQSDWMLMLYFAHTHLTVTVTIGLLLIPK--FSHSSNNPRDDIATEAYE 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sixty six Drosophila Melanogaster G-protein coupled receptors (GPCR), useful in the treatment and diagnosis of GPCR-related conditions and for identifying GPCR modulators for use as insecticides -
                                                                                                                                                                                                                                                                    DELDMGRSGSYLNSSINSAWSEHSLDPEDIRDELKKLYAQLEIYKRKKMITNNPHLQKKR
                  KVFLSRTAQRIPYMTGGRVMRMLAVILLVVFWFLIGWTSSVCQNLEK-QISLIGQGKTSD
                                                                                                                                                                                                                                GGRKAGHRRF-----SLQKKGSKDKALSAKHRSNKHHQDIEITEAEPSRTPEDSVC
CREGCPFCADDSPC--FVQE----DKYLRLAIISFQGLCMLLDFVSMLVVYHFRKAKSI
                                                      RASGLILLETILFGSLLLYFPVVILYFEPSTFRCILLRWARLLGFATVYGTVTLKLHRVL
                                                                                                                                  358 VDFRTRKAHRW-VLRDVDLLKYLGTMVFAVICYMAAFTASSLDLLESAOLESLREADT--
                                                                                                                                                              HLIFNMCLIDRWDYMTAVAEFLFLLWGVYLCYAVRTVPSAFHEPRYMAVAVHNELIISAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila G-protein coupled receptor, GCPR #61
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                                                                                                                                                                                                                                                                                                                                                                                             SAEGPTDTYAEISGVSHSMLSHSMVSH 662
                                                                                                                                                                                                                                                                                                                                                                           TGKSKEETLK -- NRVFSLKKSHSTYDH 823
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2000US-0618893.
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18-JUL-2000;
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                                                                                                                                                                            110 GKWPALASAHPSLHRALDTLTHATNFLNVMLQSNKSREQNLQDDLDWYQALVWSLLEGGFP 169
                                                                                                                                                                                                                               SISRAAITFSTDSLSAPAPQVFLQATREESRILLQDLSSSAPHLA-----NATLETEWF 223
                                                                                                                                                                                                                                                                                                             HNKAYLGSYWRE------LGAAWNSTDGTQ-----EWGAPFRDCNLLTRRWL 139
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conditions. The GPCR proteins and nucleic acids are also useful for identifying modulators of GPCR proteins for use as insecticides. The nucleic acid can also be used to detect mutations in GPCR genes and expression products such as mRNA. AAJ38923-AAJ38988 represent D. melanogaster G-coupled protein receptor amino acid sequences of
                                                                                                                                                                                                  GKWPC-RMFYDYTDIAEDAARQFIEFL-----EP
                                                                                                                                                                                                                                                          --TRAEVSRRANGIAS-----YALNEDDNLLAFAIAAPSIHTVVVKFRDNVTIPPDQV
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Droscophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                         TTENSTLESLSGKKLTQKLKEDSEAESTESVPLVCKSASAHNLSSEKKTGHPRTSMLQKS
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                                                         Drosophila; developmental biology; cell signalling; insecticide;
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                   Drosophila melanogaster polypeptide SEQ ID NO 36720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from prosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                        649
                                                                                                                    LAWGVRLCIMVRKAPSEFNESRFISMAIYNEFLLTCFLNVSMLFLQSPANPDLLYIIFFC 170
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                                                                                        LIMGVYLCYAVRTVPSAFHEPRYMAVAVHNELIISAIFHTIRFVLASRLQSDWMLMLYFA
MYPNPNLYTCTARIWLREIGFSLTYGALMLKTWRISVIFRVRSAKAVK-ITDAALLKRLG
                                                VILLVVFWFLIGWTSSVCQNLEKQISL--IGQGKTSDHLIFNMCLIDRWDYMTAVAEFLF
                                                                                                                                                                                                                                                                                                                                                                              Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 14637; 21pp + Sequence Listing; English.
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Pred. No. 2.2e-09;
5; Mismatches 496;
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                                                                                                                                                                                                                                                                SWRRKDGLGGDKSHF----KWSPPYLEC-ENGSYKPGWLVTLSSAIYGLQPNLVPEFRG 302
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260 YSTDWWNVTQDSECSVEE-----IATALEG-----AILVDLLPLSTSGDIT
                                                                                       191 FLQATREESRILLQDLSSSAPHLANATLETEWFHGLRRK--WRPHLHRRGPNQGPRGLGH
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VMKVDINLQKVDIDQCSSDGWFSGTHKCHLNNSECMPIKGLGFVLGAYECICKAGFYHPG 362
                                  - RKANILINOFOLGOMEKIGEYH - SOKSHLDLSLGKPVKWVG -
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                                                                                                                                                                              Drosophila; G-protein coupled receptor; GCPR; insecticide; diagnostic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QKLAEEVPMDVASYLYTGDSHQLKRANCSG-RYELAGLPGKWPALASAHPSLHRALDTLT 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                Sixty six Drosophila Melanogaster G-protein coupled receptors (GPCR), useful in the treatment and diagnosis of GPCR-related conditions and for identifying GPCR modulators for use as insecticides
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 ----EVCP 1173
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4.0%; Score 254; DB 22;
Best Local Similarity 17.9%; Pred. No. 2.2e-09;
Matches 213; Conservative 195; Mismatches 496;
                                                                                                                                                       Drosophila G-protein coupled receptor, GCPR #20
 NQIGHQEKK - - - TSSSEENVRGSYNSSNNFQQPLTSRA -
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                                                                                 AAU38942 standard; Protein; 1221
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2000US-0618893.
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N-PSDB; AAS57110, AAS57111.
                                                                                                                                 (first entry)
                                                                                                                                                                                                                 Drosophila melanogaster.
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                                                                                                                                                                                           mutation detection
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18-JUL-2000;
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949 SGGDCSSMRERRQSTASRHYDSGSQTPTARPKYSSSHRNSSTNISTSQSELSNMCPHSKP 1008 RKPQKSGIMKQQRVNPTTANSDLNPGTTQMKDNFDIGEVCPWEVYDL-----TPGPVP 1020 SPORCAEHHGGHGMTYDPNTTSPIORSVSEKNRNKHRPKP------OKGTVC-- 1107 STP---AVIK----TPTASDHRRTSMGSALKSNFVVSQSDLWDTHTLSHAKQRQSPRNYA 1061 SESKVQKHVSIVASEMEKNPT-----FSLKEKSHHKPKAAEVCQQSNQKRIDKAEVCLW 1074 ESQGQSILEDEKLLISKTPVLPERAKEENGGQPRAANVCAGQSEELPPKAVASKTENENL 1134 QSETDSERERDPPPNSQPCVQPRKVS-----RSSNIQHAAHHHSSPNVAPDK---QRS 1157 ----DRTLIYIEHSOVNPTIYIV 450 LAIISFQGLCMLLDFVSMLVVYHFRKAKSIRASGLILLETILFGSLLLYFPVVILYFEPS 477 -----TFRCILLRWARLLGFATVYGTVTLKLHRVLKVFLSRTAQRIPYMTGGRVMRML 530 509 ISSVAAFPYICTARAWILMAGFSLSFGAMFSKTWRVHSIFTDLKLNK-KVIKDYQLFMVV 567 AVILLVVFWFLIGW-TSSVCQNLEKQISLIGQGKTSDHLIFNMCLIDRWDYMTAVAEFLF 589 AWSEHSLDPEDIRDELKKLYAQLEIYKRKKMITN-NPHLQKKRCSKKGLGRSIMRRITEI 761 762 PETVSRQ-----CSKEDKEGADHGTAKGTALIRKNPPESSGNTGKSKEETLKNRVFSLK 815 PE--ARKWIDGVTCTGGSNVGSELEPILNDDIVRLSAPPVRREMPSTTEVTEMTSVDSVT 836 816 KSHSTYDH---VRDQTEESSSLPTESQEEETTEN-----STLESLSGKKLTQKLKEDSE 866 MODOH-----LOQQQHQQQQQQQQQQQHHHRHLEKRNSVSAQTDD----NIGSITSTAGKR 948 GVLLAIDIAIITTWQIADPFYRETKQLEPLHHENIDDVLVIPENEYCQSEHMTIFVSIIY -----LLWGVYLCYAVRTVP-SAFHEPRYMAVAVHNELIISAIFHTIRFVLASRLQSDW STHVEMDINSFVSVQSTVMAPSLPPKKKKQSIVEHHSHAPAPTMMQPIQQQLQQHLQQHQQ AESTESVPLVCKSASAHNLSSEKKTGHPRTSMLQKSLSVIASAKEKTLGLAGKTQTAG-----SQKPLPKDKETNRNHSNSDNTETKDPAPQNSNPAEEP SASASVIGVIIATVFLAFNIKY - - RNQRYIKMSSPHLNNLIIVGCMMTYLSIIFLGLDTT MLMLYFAHTHLTVTVTIGLLLIPKFSHSSNNPRDDIATEAYEDELDMGRSGSYLNSSINS VLPVNNFRRRGPDQHISGSTKDVSEEAYVCLPCREGCPFCADDSPCFVQEDK--NOIGHOEKK ---TSSSEENVRGSYNSSNNFOOPLISRA----

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                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel polypeptide (I), functioning as a gamma-aminobutyric acid -B (GABA-B) receptor which has insecticidal activity. (I), also the nucleic acid (II) that encodes it and related vectors, host cells, antibodies and transgenic invertebrates, are used for identifying: (i) new plant protection agents, i.e. modulators of (I) with insecticidal activity, which may also be useful in human or veterinary medicine; and (ii) genes that encode polypeptides involved in assembly of functionally related GABA-B receptors in insects. This sequence represents a fruitily (Drosophila melanogaster) GABA-B receptor which is described in the method of the invention.
                                                                                                                                                                                                                                                                                                           invertebrate gamma-aminobutyric acid receptor proteins, useful in sening for potential insecticides, for plant protection or medicine,
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                                  GABA-B receptor; fruitfly; gamma-aminobutyric acid B receptor insecticide; transgenic invertebrate; plant protection agent; human medicine; veterinary medicine; insect.
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            melanogaster GABA-B receptor protein SEQ ID 4.
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17.5%; Pred. No. 1.3e-08;
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Matches 212; Conserv
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SASASVIGVIIATVFLAFNIKY - - RNQRYIKMSSPHLNNLIIVGCMITYLSIIFLGLDTT
                                                             ----TERCILLRWARLLGFATVYGTVTLKLHRVLKVFLSRTAQRIPYMTGGRVMRML
                                                                                                    LSSVAAFPYICTARAWILMAGFSLSFGAMFSKTWRVHSIFTDLKLNK-KVIKDYQLFMVV
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                                                                                                                                                                                                                                                                                                                                                                                                                          4;
                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention sequences genomic DNA sequences (ABL16176-ABL30511), expressed DNA (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                 WIPO
                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |:|: || || :: : | : : | :: | :: | CLCRKGFYFPDIVSQHKF-----FNGSLLEEEYEKLMLGKNSTYNSNSEYECLPCAE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----SEEAYVCLPCRE 397
                                                                                                                                                                                                                                                                                                                                                                                                                                            301 RGVMKVDINLQKVDIDQCSSD-----GWFSGTHKCHLNNSECMPIKGLGFVLGAYE 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                         33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GABA-B receptor; fruitfly; gamma-aminobutyric acid B receptor; insecticide; transgenic invertebrate; plant protection agent; human medicine; veterinary medicine; insect.
                                                                                                                                                                                                                                                                                                                                                                                                     Length 176;
                                                                                                                                                                                                                          Disclosure; SEQ ID NO 28347; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                 Score 238.5; DB 22; Length
Pred. No. 1.7e-09;
5; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCPFCADDSPCFVQEDKYLRLAIISFQGLCMLLDFVSMLVVYHFR 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         melanogaster GABA-B receptor protein SEQ ID
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                                                                                                                               Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB86161 standard; Protein; 1305
                                                                                                                                                                                                                                                                                                                                                                                                  / Match 3.7%; Sc
Local Similarity 31.5%; Pr
nes 52; Conservative 25;
                                                                                                                              PWD,
                                                  23-MAR-2001; 2001WO-US09231.
                                                                        23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
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                                                                                                                             Venter JC, Adams M,
                                                                                                                                                 WPI; 2001-656860/75.
                                                                                                       (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                               176 AA;
                                                                                                                                                            N-PSDB; ABL11288
         WO200171042-A2
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                                                                                                                                                                                                      interactions
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This invention describes a novel polypeptide (I), functioning as a gamma-aminobuytric caid = B (GABA-B) receptor which has insecticidal activity. (I), also the nucleic acid (II) that encodes it and related vectors, host cells, antibodies and transgenic invertebrates, are used for identifying: (i) new plant protection agents, i.e. modulators of (I) with insecticidal activity, which may also be useful in human or veterinary medicine; and (ii) genes that encode polypeptides involved in sasembly of functionally related GABA-B receptors in insects. This sequence represents a fruitfly (Drosophila melanogaster) GABA-B receptor which is described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New invertebrate gamma-aminobutyric acid receptor proteins, useful in screening for potential insecticides, for plant protection or medicine, also related nucleic acid -
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Pred. No. 1e-07;
3; Mismatches 396;
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18.6%;
99DE-1055408
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18-NOV-1999;
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LLVTLWVVTDPMERHLHNLTLEIS----ATDRSVVYQPQVEVCRSQHTQTWLSVLYAYK 808
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                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16175) and the encoded proteins RAB57137-ABB72072).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 3.6%; Score 227.5; DB 22; Best Local Similarity 18.8%; Pred. No. 2.2e-07; Matches 209; Conservative 171; Mismatches 381;
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      PWD,
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      Adams M,
                                                                                                                       2001-656860/75
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                                                                                                                                                                                     N-PSDB; ABL03600
                                                                                                                                                                                                                                                                                                                                                                                                                                   interactions
Venter JC,
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The invention relates to sixty six novel isolated Drosophila melanogaster G-protein coupled receptors (GPCR). The GPCR proteins and nucleic acids are useful in the treatment and diagnosis of GPCR-related
                                                                             | : | | | : | : | : | AASKNRTPSISG-----ILPNLILSVLPPVIPRASWPSAEYMQIPMRRSVTFASQPQ 1043
                                                                                                                                                    ----ACLPAQDLINLRLAHQQATEAKTG 1070
                                                                                                                                                                                                                                                                 LINRLRGIFSRTTSSNKG-STASLADQKGLKAAFKSH-MGLFTRL----IPSSQTASCN 1123
                                                                                                                                                                                                                                                                                                                                       1174 IPTISGGEQGDQTLG-----GKYVKLLETKVNFQLPSNRRPSVVQQPPSLRERVRGS 1225
                                                                                                                                                                                                                                                                                                                                                                                                      PRFPHRILPPTCSLS------ALAESEDRP--GDSTSILGSCKSIPRISLOOATSG 1273
                                                                                                                                                                                                                                                                                                           IGEVCPWEVYDLTPGPVPSESKVQKHVSIVASEM-----EKNPTF----SLKEKSHHK 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila; G-protein coupled receptor; GCPR; insecticide; diagnostic; mutation detection.
                                                                                                                                                                                    944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sixty six Drosophila Melanogaster G-protein coupled receptors (GPCR), useful in the treatment and diagnosis of GPCR-related conditions and for identifying GPCR modulators for use as insecticides -
TNNPHLQKKRCSKKGLGRSIMRRITEIPETVSRQCSKEDKEGADH------GTAKGT
                           ----IQALDAEIRKLERLLESGLTTTSTTTSSSTSL--LTGGGHLKPELTVTSGISQTP
                                                                                                                                                                                  ------HPRTSMLQKSLSVIASAKEKTLGLAGKTQTAGVEERTKSQKPLPKDKETNRN
                                                                                                                                                                                                                                            HSNSDNTETKDPAPQNSNPAEEPRKPQKSGIMKQQRVNPTTANSDLNPGTTQMKD-NF-D
                                                          ALIRKNPPESSGNTGKSKEETLKNRVFSL-----KKSHSTYDHVRDQTEESSSLPTESQ
                                                                                                                        -AHNLSSEKKTG
                                                                                                                                                                                                                                                                                                                                                                       PK----AAEVCQQSNQKRIDKAEVCLWESQGQSILEDEKLLISKTPVLPERAKEE--NG
                                                                                                                     EEETTENSTLESLSGKKLTQKLKEDSEAESTESVPLVCKSAS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila G-protein coupled receptor, GCPR #5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAU38927 standard; Protein; 1305
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18-JUL-2000;
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                                                                                                                                                                                                                                          ------HPRTSMLQKSLSVIASAKEKTLGLAGKTQTAGVEERTKSQKPLPKDKETNRN 944
                                                                                                                                                                                                                                                                                                                       443 QFH-----GQDGFGSGYGSRISIAATQSDSRRRRRGVGGTSGGHLFPEAISQYAPQTY 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----ADDSPCFVQEDKYLRLAIISF 423
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                                                                                                                                                                                        Gaps
conditions. The GPCR proteins and nucleic acids are also useful for identifying modulators of GPCR proteins for use as insecticides. The nucleic acid can also be used to detect mutetions in GPCR genes and expression products such as mRNA. AAU38923-AAU38988 represent D. melanogaster G-coupled protein receptor amino acid sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----LHDIWARNDIIDPVIHSMGLKMECNTRRFVVDDRRELQYRVEVQURVYKKE---
                                                                                                                                                                                                                                                                                                                                                          278 KPGWLVTLSSAIYGLQPNLVPEFRGVMKVDINLOKVDIDQCSSDGWFSGTHKCHLNNSEC
                                                                                                                                                                                                                                                                                                                                                                                           -----RAAEEHW------RRNEEO
                                                                                                                                                                                                                                                                                                                                                                                                                            338 MPIKGLGFVLG--AYECICKAGFYH-PGVLPVNNFRRRGPDQHISGST-----KDVSEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                           520 SKLDGFDYTRSDMAWEFLQQMGKLHFLGVSGPVSF--SGPDR--VGTTAFYQIQRGLLEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          576 VALYYPATDALDFRCPRCRPVKWHSGQVPIAKRVFKLRVATIAPL----AFYTIATLSS
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                                                                                                                                                       Length 1305;
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                                                                                                                                                     ore 227.5; DB 22;
ed. No. 2.2e-07;
Mismatches 381;
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                                                                                                                                                     Score 227.5;
Pred. No. 2.2
                                                                                                                                                                                    Conservative 171;
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18.8%;
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                                                                                                                    Sequence 1305 AA;
                                                                                                                                                                     Similarity
                                                                                      the invention.
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HSNSDNTETKDPAPQNSNPAEEPRKPQKSGIMKQQRVNPTTANSDLNPGTTQMKD-NF-D 1002
                             IGEVCPWEVYDLTPGPVPSESKVQKHVSIVASEM-----EKNPTF----SLKEKSHHK
                                                         PK----AAEVCQQSNQKRIDKAEVCLWESQGQSILEDEKLLISKTPVLPERAKEE--NG
                                                                                                                                                                                               Xenopus occyte; cerebellum sublibrary; voltage clamp assay; neurotransmitter; glutamate; neuronal excitation; clone 45-A.
                                                                                                                                                                                                                                                                                                          Transmembrane_domain
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                                                                                     GQPRA-----ANVCAGQSEELPPKAVASKTE 1130
                                                                                              'note= "N-glycosylation"
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91US-0648481.
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18-MAR-1991;
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                                                                                                                                                                                                                                                                                               Mammalian G protein-coupled glutamate receptors - activate phospholipase C or stimulate inositol phospholipid metabolism, for use in diagnosis and identification of receptor agonists and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.5%; Score 223.5; DB 13; Length 1199; ilarity 18.6%; Pred. No. 3.8e-07; Conservative 121; Mismatches 325; Indels 271;
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                                                                                                                                                                                                                                                                                                                                                                                       Chimeric receptor; extracellular domain; seven transmembrane domain; intracellular cytoplasmic tail domain; metabotropic glutamate receptor; MGR; calcium receptor; CR; mGluR; G protein-coupled receptor; neurological disease.
                                                                                                                                                               -----LRSLYPPPPPPQHLQMLPLHLSTFQEESISPPGEDIDDDS--- 1108
                                                                                                                                               1052 PKAAEVCQQSNQKRIDKAEVCLWESQG---QSILEDEKLLISKTPVLPERAKEENGGQPR 1108
                                                                                                994 TIQMKDNFDIGEVCPWEVYDLIPGPVPSE--SKVQKHVSIVASEMEKNPTFSLKEKSHHK 1051
LSSEKKTGHPRTSMLQKSLSVIASAKEKTLGLAGKTQTAGVEERTKSQKPLPKDKETNRN 944
                       RGPPVATTPPLPPHL------TAEETPLFLADSVIPKGL-----PPPLPQQQ----
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                                              HSNSDNTETKDPAPQNSNPAEEPRKPQKSGIMKQQRVNPTTANSDL------NPG
                                                                                                                                                                                                                1109 AANVCAGQSEELPP--KAVASKTENENLNQIGHQEKKTSSS 1147
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                                                                                                                                               311 QKVDIDQCSSDGWFSGTHKC---HLNNSE-CMPIKGLGFVLGAYECICKAG---FYHPGV 363
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                                                                                                                                                                                                                                                                                                   364 LPVNNFRRRGPDQH-----ISGSTKDVSEE----AYVCLPCREG-------CPFCAD 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DFWSNENHTSCEPIPVRYLEWSDIESIIAIAFSCLGILVTLFVTLIFVLYRDTPVVKSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --IFRRKKPGAGNANSNGKSVSWSEPGGRQAPKGQHVWQRLSVHVKTNETACNQ----
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                                                                         270;
                                                                     Conservative 127; Mismatches 354; Indels
   Length
Score 220; DB 18;
Pred. No. 7.1e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESVLCTPPNVTYASVILRDYKQSSS 1217
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3.4%;
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Job time : 76.2905 secs

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February 15, 2003, 05:55:14; Search time 32.8197 Seconds (without alignments) 3558.936 Million cell updates/sec
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

    protein search, using sw model

                                                                                              OM protein
                                                                                                                                            Run on:
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US-09-775-181-2 6382 1 MGAMAYPLLICLILAQLGLG......LSANKIAGPRKEEIWDSFKV 1215 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

Atal number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries fimum DB seq length: 0 Maximum DB seq length: 2000000000

pir1:\* pir2:\* pir3:\* PIR\_73:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ES	Description	hypothetical prote		G protein-compled		metabotropic gluta	protein UNC-89 - C	neurofilament prot	- 17			trfA protein - sli	Ω	hypothetical prote		_	_	SIR4 protein - yea	ā	•—	hypothetical prote	IgA-specific metal	triadin - human	ankyrin 2, neurona	hypothetical prote	cylicin I - bovine	hypothetical prote	•	probable nuclear p
SUMMARIES	ΩI	T21989	T13564	A41939	A42916	JC2132	T29757	A46194	JC2131	T34418	B42680	T14004	A86827	T29776	C96608	T06310	T42727	A29360	T22458	F95133	T29108	B98002	S68191	S37431	T06029	A40713	T16420	S33124	T41023
	DB	7	~	8	~	7	7	7	7	7	7	7	~	7	7	7	7	7	7	7	7	7	7	7	7	~	7	~	~
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di	Query	4.4	3.5	9.2	м М	3.3	3.5	3.2					2.9				5.9		2.8		2.8				2.8			2.8	2.7
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RESULT T13564

neurofilament trip hypothetical prote ribonuclease E (EC nucleolar phosphop junctional sarcopl calcium/polyvalent glutamate receptor probable involveme hypothetical prote metabotropic gluta metabotropic gluta hypothetical prote pypothetical prote cylicin I - human neurofilament trip ribonuclease E NMB	al protein F39B2.8 - Caenorhabditis elegans Caenorhabditis elegans -oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000 n: T21989 R. to the EMBL Data Library, March 1997 to the EMBL Data Library, March 1997 n: T21989 n: T21989 preliminary; translated from GB/EMBL/DDBJ preliminary; translated from GB/EMBL/DDBJ rights n: T21989 preliminary; translated from GB/EMBL/DDBJ preliminary; translated from GB/EMBL/DDBJ rights n: T21989 preliminary; translated from GB/EMBL/DDBJ preliminary; translated from GB/EMBL/DDBJ rights n: T21989 preliminary; translated from GB/EMBL/DDBJ loss	YLMSSINSAWSE-HSLDPEDIRDELKKL 72    : .   ::        ::3  ILNGTIDFAEVPIADMNPEDIRAELKRV 34  IMRRITEIPETVSRQCSKEDK 774    ::         :    RATRRIS-IPSCSPQTK 393
OFHUH T29233 F51198 F51198 F51198 A45990 F59362 T40315 T40431 T34036 T22457 B84683 B40713 A27864 F811225	protein F39B2.8 - Caenorhabdit aenorhabditis elegans 721999 #sequence_revision 15-0 721989 tsequence_revision 15-0 721989 tsequence_revision 15-0 721989 tsequence_revision 15-0 721989 tsequence_revision 15-0 721989 translated from GB/EP 1433 cwills and source: EMBL: 292834; PIDN: CABO7 al source: EMBL: 292834; PIDN: CABO7 al source: Clone F39B2 al source: Clone F39B2 al source: Clone F39B2 al source: Line 129B2.8 al similarity 28.78; Pred: No. 02; Conservative 57; Mismat ILFGSLLLYFPVILYFEP-1	RDDIATEAYEDELDMRRSGS SRRSWTLGGHSGRAHPSLAKLRDN AQLEIYKRKMITNNPHLQKKRCSKKGLGRS    :     :       :::: TQLRWYKLKNLYQDNPHISKKRGGKKWSDKN
наиминичения при	B - Cael legans ce_revii. Library Library 2834; P e F3982 e F3982 y Y/3; 33 is elegans ll :: AQHVS-V MCLIDR REVLAGR REVLAGR REVLAGR REVLAGR RESIRNS RSG	GRSG   1  GHSGRAHP PHLQKKRC   : 1   PHISKKRG
1020 1558 919 919 910 706 1079 11310 971 1359 879 879 879 904 916	al protein F39B2.8 - Gaenorhabditis elega Caenorhabditis elega Not 121989 #sequence_rn r21989 #sequence_rn r21989 #sequence_rn r21989 #sequence_rn r21989 #sequence r1948 #sequence r1948 #sequence r1948 #sequence r1948 #sequence r1949 #seq	ELDMGRSG 
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997 MKDNFDIGEVCPWEVYDLTPGPVPSE--SKVQKHVSIVASEMEKNPTFSLKEKSHHKPKA 1054
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G protein-coupled glutamate receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Accession: A41939; S15362
R;Houamed, K.M.; Kuijper, J.L.; Gilbert, T.L.; Haldeman, B.A.; O'Hara, P.J.; Mulvihill, Science 252, 1318-1321, 1991
microtubule-associated protein homolog - fruit fly (Drosophila melanogaster)
N;Alternate names: hypothetical protein EG:49E4.1
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 17-Nov-2000
C;Accession: T13564
R;Spanos, L.; Papaglannakis, G.; Siden-Kiamos, I.; Louis, C.
Spanos, L.; Papaglannakis, G.; Siden-Kiamos, I.; Louis, C.
A;Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A;Reference number: 217689
A;Accession: T13564
A;Accession: T13564
A;Accession: T13564
A;Accession: T13564
A;Molecule type: DNA
A;Residues: DNA
A;Residues: 1-5327 <SPA>
A;Cross-references: EMBL:AL031128; PIDN:CAA20006.1
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                                                                                                                                                                                                                                                                                                                     Cross-references: FlyBase:FBgn0025392
Introns: 24/2; 52/3; 104/3; 179/1; 232/1; 1669/3; 2566/1; 4798/3; 5272/1
Note: EG:49E4.1
Uperfamily: Drosophila 576K microtubule-associated protein homolog
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A;Title: Cloning, expression, and gene structure of a G protein-coupled glutamate
A;Reference number: A41939; MUID:92022526; PMID:1656524
A;Accession: A41939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----AYVCLPCREG- 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  399 ------CPFC-----ADDSPCFVQEDKYLR-----LAIISFQGLCMLLDFVSMLVV 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----ASTKTLYNVEEEDNTPSAHFSPPSSPSSMVVHR 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      885 LSSEKKTGHPRTSMLQKSLSVIASAKEKTLGLAGKTQTAGVEERTKSQKPLPKDKETNRN 944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         498 GTWHEGVLNIDDYKIQ---MNKSGMVRSVCSEPCLKGQIKVIRKGEVSCCWICTACKENE 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                499 VILKLHRVLKV-------FLSRTAQRIPYMTGGRVMRMLAVILLVVFWFLIGW 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     765 VSRQCSKEDKEGADHGTAKGTALIRKNPPESSGNTGKSKEETLKNRVFSLKKSHSTYDHV 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      825 RDQTEESSSLPTESQEEETTENSTLESLSGKKLTQKLKEDSEAESTESVPLVCKSASAHN 884
                                                                                                                                                                                                                                        PID:9204460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PID:956647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            439 YHFRKAKSIRASGLILLETILFGSLLLYFPVVILYFEPSTFRCILLRWARLLGFATVYGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                545 TSSVCQNLEKQISLIGQGKTSDHLIFNMCLIDRWDYMTAVA-EFLFLLWGVYLCYAVRTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSAFHEPRYMAVAVHNELIISAIFHTIRFVLASRLQSDWMLMLYFAHTHLTVTVTIGLLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PANFNEAKYIAFTMYTTCIIWLAFVPIYF -----GSNYKIITTCFAVSLSVTVALGCMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       664 IPK----FSHSSNNPRDDIATEAYEDELDMG------RSGSYLNSSINSAWSEHSLDP
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A.Molecule type: nucleic acid
A.Rolecule type: nucleic acid
A.Rolecule type: nucleic acid
A.Cross-references: GB.MG1099; NID:g397806; PIDN:AAA19497.1; PID:g2044
A.Experimental source: cerebellum
A.Note: sequence extracted from NCBI backbone (NCBIP:60785)
R.Masu, M.; Tanabe, Y.; Tsuchida, K.; Shigemoto, R.; Nakanishi, S.
Nature 349, 760-765, 1991
A.Title: Sequence and expression of a metabotropic glutamate receptor.
A.Reference number: S15362; MUID:91156047; PMID:1847995
A.Stocession: S15362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDIRDELKKLYAQLEIYKRKKMITNNPHLQKKRCS-----KKGLGRSIMRRITEIPET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    675 LVTKTNRIARILAGSKKKICTRKPRFMSAWAQVIIASILISVQLTLVVTLII-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-1199 <MAS>
A;Cross-references: EMBL:X57569; NID:g56646; PIDN:CAA40799.1;
C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSNSDNTETKDPAPQNSNPAEEPRKPQKSGIMKQQRVNPTTANSDL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 3.5%; Score 220.5; DB 2; Best Local Similarity 18.6%; Pred. No. 0.00026; Matches 163; Conservative 120; Mismatches 330;
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human
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A; Molecule type: mRNA
A; Residues: 1-1180 <MIN>
C; Comment: This protein is coupled to guanine nucleotide binding proteins.
C; Keywords: glycoprotein; neurotransmitter; receptor; transmembrane protein
F; S80-604/Domain: transmembrane #status predicted <TMI>
F; 617-637/Domain: transmembrane #status predicted <TM3>
F; 644-664/Domain: transmembrane #status predicted <TM4>
F; 647-647/Domain: transmembrane #status predicted <TM4>
F; 738-759/Domain: transmembrane #status predicted <TM5>
F; 738-759/Domain: transmembrane #status predicted <TM6>
F; 773-794/Domain: transmembrane #status predicted <TM6>
                                                                                                                                                                                                                                                                971 EESFPAAARPRSPSPISTLSHLAG-----SAGRTDDDAPSLHSETAARSSSSQGS 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of two isoforms of
                                                                                                                                                                                                                                                                                                                                                                                                                                   ERNVRSAFTTSTVVRMHVGDGKSSSAASRSSSLVNLWKRRGSSGETLSSNGKSVTWAQNE 888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ETEWFHGLRRKWRPHLHRRGPNQGPRGLGHSWR-----RKDGLGGDKSHFKWSPPYLECE 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVKWFDDYYLKLRPETNHRNP----WFQEFWQHRFQCRLEGFPQENSKYNKT----CN 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NG------SYKPGWLV-TLSSAIYGL---QPNLVPEFRGV-------MKVDINLQ 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSLTLKTHHVQDSKMGFVINAIYSMAYGLHNMQMSLCPGYAGLCDAMKPIDGRKLLESLM 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------KDYFDYINVGSWDNGEL 492
                                                                                                                                                                                 ----LYDVAEA
                                                                                                                                                                                                                        SSSLPTESQEEETTENSTLESLSGKKLTQKLKEDSEAESTESVPLVCKSASAHNLSSEKK
                                              -----LYAQLEIYKRKKMITNNPHLQK---KRCSKKGLGRSIMRRITEIPETVSRQCS
                                                                                          --- PGAAAGGGS
                                                                                                                                    771 KEDKEGADHGTAKGTALIRKNPPESSGNTGKSKEETLKNRVFSLKKSHSTYDHVRDQTEE
                                                                                                                                                                                                                                                                                                                 --KTQTAGVEER
                                                                                                                                                                                                                                                                                                                                                                                                     TKSQKPLPKDKETNRNHSNSDNTETKDPAPQNSNPAEE-PRKPQKSGIMKQQRVNPTTAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KVDIDQCSSDGWFSGTHKCHLNNSECMPIKGLGFVLGAYECICKAGFYHPGVLPVNNFRR
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                                                                                                                                                                                                                                                                                                                                                      LMEQISSVVTRFTANISELNSMMLSTAATPGPPGTPICSSYLIPKEIQLPTMTTFAE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C. Accession: JC2132
R.Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, Blochem. Blophys. Res. Commun. 199, 1136-1143, 1994
A.Title: Molecular cloning and the functional expression of two iss A.Reference number: JC2131; MUID:94197696; PMID:7908515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.3%; Score 210; DB 2; Length 1180;
llarity 19.1%; Pred. No. 0.00098;
Conservative 120; Mismatches 400; Indels 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --AYVCLPCREG---
                                                                                        KSTRGOHLWQRLSVHINKKENPNOTAVIKPFPKSTENRG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----FRDSVDSGSTTPNSPVSESALCIPSSPK 1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDLNPGTTQMKDNFDIGEVCPWEVYDLTPGPVPSESK 1024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          metabotropic glutamate receptor 5 A - human
                                                                                                                                                                            937 GPGVAGA -- GNAGCTATGGPEPPDAGPKA-
                                                                                                                                                                                                                                                                                                                 TGHPRTSMLQKSLSVIASAKEKTLGLAG--
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Matches 179; Conserv
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A;Residues: 1-1171 <ABE>
A;Cross-references: GB:D10891; NID:g220813; PIDN:BAA01711.1; PID:d1002186; PID:g220814
                                                                                                                                                                                                                                                                                                                                                                                                                                                 mGluR5
                                                                                                                                                                                                                                                                                                                                                                                              R;Abe, T.; Sugihara, H.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi, S. J. Biol. Chem. 267, 1336-13368, 1992
A:Title: Molecular characterization of a novel metabotropic glutamate receptor preference number: A42916; MUID:92317054; PMID:1320017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                35;
                                                                                          C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Mar_1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ETEWFHGLRRKWRPHLHRRGPNQGPRGLGHSWR-----RKDGLGGDKSHFKWSPPYLECE 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DVKWFDDYYLKLRPETNLRNP-----WFQEFWQHRFQCRLEGFAQENSKYNKT-----CN 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NG-----SYKPGWLV-TLSSAIYGL---QPNLVPEFRGV-------MKVDINLQ 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KVDIDQCSSDGWFSGTHKCHLNNSECMPIKGLGFVLGAYECICKAGFYHPGVLPV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----NNFRRGPDQHI-SGSTKDVSEE----AYVCLPCREG------CPFC----A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDLTGCDLIPVQYLRWGDPEPIAAVVFACLGLLATLFVTVIFIIYRDTPVVKSSSRELCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TILFGSLLLYFPVVILYFEPSTFRCILLRWARLLGFATVYGTVTLKLHRVLKV-----
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                                                                 AEVCQQSNQKRIDKAEVCLWESQG---QSILEDEKLLISKTPVLPERAKEENGGQPRAAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 19.1%; Pred. No. 0.00097;
Matches 179; Conservative 117; Mismatches 397; Indels 244;
Length 1171;
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C;Keywords: G protein-coupled receptor; transmembrane protein
                                                                                                                                                     1112 VCAGQSEELPP--KAVASKTENENLNQIGHQEKKTSSS 1147
                                                                                                                                                                                   1160 VASGSSVPSSPVSESVLCTPPNVTYASVILRDYKQSSS 1197
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A;Map position: 1
A:Introns: 17/2: 108/3: 154/2: 211/2: 265/3: 326/2: 352/3: 426/2: 454/1: 500/1: 537/1;
/3: 5917/1: 6027/1: 6061/3: 6153/2: 6515/1: 6552/3: 6609/1
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C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: 15-oct-1999 #sequence_revision 15-oct-1999 #text_change 03-Dec-1999
C; Accession: T29757
R; Du, Z.; Le, T.T.; Wilson, R.
submitted to the EMBL Data Library, May 1997
B; Description: The sequence of C. elegans cosmid C09D1.
A; Reference number: 220679
A; Accession: T29757
A; Accession: T29757
A; Accession: T29757
A; Molecule type: DNA
A; Residues: 1-6642 < DUZ>
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A; Residues: 1-6642 < DUZ>
A; Cossion: T29757
A; Cos
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                                                 SSRELCYIILAGICLGYLCTFCLIAKPKQIYCYLQRIGIGLSPAMSYSALVTKTNRIARI
                                                                                                           -------FLSRTAQRIPYMTGGRVMRMLAVILLVVFWFLIGWTSSVCQNLEKQ
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; Pred. No. 0.021;
98; Mismatches 270;
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                                                                                                                                                                673 LAGSKKKICTKKPRFMSACAQ----
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22.4%;
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Matches 151; Conservative
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C; Species: Loligo pealeii (longfin squid)
C; Date: 22-Sep-1993 #sequence_revision 25-Apr-1997 #text_change 17-Mar-2000
C; Accession: A46194
R; Way, J; Hellmich, M.R.; Jaffe, H.; Szaro, B.; Pant, H.C.; Gainer, H.; Battey, J. Proc. Natl. Acad. Sci. U.S.A. 89, 6963-6967, 1992
A/Title: A high-modecular-weight squid neurofilament protein contains a lamin-like r. A; Reference number: A46194; MUID:92357751; PMID:1379729
A; Accession: A46194
A; Status: nucleic acid sequence not shown; not compared with conceptual translation A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-1200 cWAY>
A; Cross-references: GB:M94389; NID:g161291; PID:g161292
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1397 TKKTGEEVKSPKEKSPASPT-----KKEKSPAAEEVKSPTKK-----EKSPSS---P 1440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                          1287 TIMSTIEVTSTVGGVTVETKESESESATTVIGGGSGGVTEGSISVSKIEVVSKTDSQTDV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : : | | : : | | : | | : | | : | | EKSAEEKPKSPTKESSPVKMADDEVKSP--TKKEKSPEKVEEKPASPT--KKEKTPEKS
                                                                                                                                                                                                                         RDELKK---LYAQLEIYK-----RKKMITNNPHLQKKRCSKKGLGRSIMRRITEIPETV
                                                                                                                                                                                                                                                                                           ---TEEKPASP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DQTEESSSLPTESQEEETTENSTLESLSGKKLTQKLKEDSEAESTESVPLVCKSASAHNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1658 SPEKVEEKPISPIKKESSPIKKIDDEVKSPIKKEKSPQIVEEKPASPIKKE----KSPEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1136 QIGHQEKKTSSSEENVRGSYNSSNNFQQPLTSRAEVCPWEF-ETPAQPNAGRSVALPASS
                                                                                               HSSNNPR----DDIATEAYEDELDM-----GRSGSYLNSSINSAWSE--HSLDPE-DI
                                                                                                                                                                                                                                                                                                                                                      SRQCSKEDKEGADHGTAKGTALIRKNPPESSGNTGKSKEETLKNRVFSLKKSHSTYDHVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---SSEKKTGHPRTSML----QKSLSVIASAKEKTLGLAGKTQTAGVEERTKSQKPLPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DKSPEK - - - - SITEEIKSPVKKEKSPEKVEEKPASPTKKEKSPEKPASPTKKSENEVKSP
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A; Note: sequence extracted from NCBI backbone (NCBIP:113499)
C; Superfamily: neurofilament triplet H protein
C; Keywords: alternative splicing
                                                                                                                                                                                                                                                                    248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --EKSHHKPKAAEVCQQSNQKRID---
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A--AEELKSPTKKE 1830
| | : : | EPKKESVVVEKQDLSS--
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SSLTLKTHHVQDSKMGFVINAIYSMAYGLHNMQMSLCPGYAGLCDAMKPIDGRKLLESLM KVDIDQCSSDGWFSGTHKCHLNNSECMPIKGLGFVLGAYECICKAGFYHPGVLPVNNFRR	450 SGLILLETILEGSLLLYFPVVILYFEPSTFRCILLRWARLLGFATVYGTVTLKLHRVLKV 509    1	HEPRYMAVAVHNELIISAIFHTIRFVLASRLQSDWMLMLYFAHTHLTVTVTIGLLLIPR-     :	721 LYAQLEIYKRKMITNNPHLOKKRCSKKGLGRSIMRRITEIPETVSRQCSKEDKEGADHG 780	1   1   1   1   1   1   1   1   1   1	1041 TFSLKEKSHHRPKAAEVCQOSNQKRIDKAEVCLMESQGOSILEDEKLLISKTPVL 1095
6 6 6 6 6 6	8	Oy Oy Dp	oy oy	90 00 00 00	OY 10 Db 10 OY 10 OY 11 OY 11 OY 11 Db 11 Db 11
:	936 678 984 731 1037	OB		85 #sequence_revision 0 31 #sequence_revision 0 32 #sequence_revision 0 33 #sequence. T Res. Commun. 199, 1136 r. JC2131; MUID:9419769 31 MRNA 2 KMNA Protein is coupled to gu protein, neurotransmitt transmembrane #status transmembrane #status transmembrane #status transmembrane #status	F:694-714/Domain: transmembrane #status predicted <tm4> F:738-759/Domain: transmembrane #status predicted <tm5> F:738-759/Domain: transmembrane #status predicted <tm5> F:738-794/Domain: transmembrane #status predicted <tm5> F:803-827/Domain: transmembrane #status predicted <tm7> Query Match  Query Match  Best Local Similarity 18.2%; Pred. No. 0.0039; Matches 204; Conservative 129; Mismatches 381; Indels 409; Gaps 45; Oy 219 ETEWFHGLRRKWRPHLHRRGPNQGRGLGHSWRRKDGLGGDKSHFKWSPPYLECE 273  ::  </tm7></tm5></tm5></tm5></tm4>

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C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Nov-2000 C;Accession: B42680; A42680; S27890; S27889; S30510; S30511 R;Meier, U.T.; Blobel, G. Cell 70, 127-138, 1992 A;Title: Nopp140 shuttles on tracks between nucleolus and cytoplasm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: mRNA
A;Residues: 32-734 <MEZ>
A;Cross.references: EMBL:M94288; NID;g205751; PIDN:AAA41719.1; PID:g205752
A;Accession: S27889
                                                                                                                                                                                                                                              A; Experimental source: clone pTM6
A; Accession: A42680
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 32-180, 0', 181-734 <ME3>
A; Cross-references: GB:M94287; NID:g205749; PIDN:AAA41718.1; PID:g205750
                                                                     ....... wopp140 shuttles on tracks between nucleolus and cytoplasm. A;Reference number: A42680; MUID:92323542; PMID:1623516 A;Accession: B42680
                                                                                                                                                                                                                                                                                                                                                                          R; Meier, U.; Blobel, G. submitted to the EMBL Data Library, May 1992 A; Description: Nopp140 shuttles on tracks between nucleolus A; Reference number: $27889 A; Recession: $27890
                                                                                                                                                                                                                            A;Cross-references: GB:M94288
                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-734 <MEI>
                                                                                                                                                                A;Status: preliminary
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hypothetical protein F12F3.3 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C.Accession: 734418
R.Fulton, B.; Wohldmann, P.
submitted to the EMBL Data Library, July 1998
A.Description: The sequence of C. elegans cosmid F12F3.
A.Reference number: 221521
A.Accession: 734418
A.Molecule type: DRA
A.Molecule type: DNA
A.Molecule type: DNA
A.Residues: 1-3488 <FUL>
A.Cross references: EMBL:U80022; PIDN:AAC25885.1; GSPDB:GN00023; CESP:F12F3.3
A.Experimental source: strain Bristol N2; clone F12F3
A.Gene: CESP:F12F3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STK---ESESKETVDEKPKKKVLKKKTEKSDSS--ISQKSETSKTVVESAGPSESETQKV 1254
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introns: 281/3; 332/1; 562/3; 600/3; 1866/3; 1944/3; 3393/1
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; Pred. No. 0.031;
81; Mismatches 228;
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Best Local Similarity 20.9%;
Matches 136; Conservative 8
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QPRAANVCAGQSEE--LPPKAVASK-----TENENLNQIGHQEKKTSSSEENVRGSYN 1156
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A;Molecule type: mRNA
A;Residues: 32-180, 'Q',181-734 <MEI2>
A;Cross-references: EMBL:M94287; NID:g205749; PIDN:AAA41718.1; PID:g205750
C;Superfamily: nucleolus-cytoplasm shuttle phosphoprotein
C;Keywords: phosphoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             818 HSTYDHVRDQTEESSSLPTESQEEETTENSTLESLSGKK-LTQKLKEDSEAESTESVPLV 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     928 RIKSOKPLPKDKETNRNHSNSDNTETKDPAPQNSNPAEEPRKPOKSGIMK-QORVNPTTA 986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | | : | | : | 346 ----SSEEEKKTPAKTVVSKTPAKPAVKK 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   398 KAE---SSSDSDSDSSEDEAPAKPVSATKSPLSKPAVTPKPPAAKAVATPKOPA---- 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                507 DSSSDSESSSSEEEKKIPPKPPAKKKAAGAAVPKPIPVKKAAAESSSSSSSSSE-----D 560
                                                                                                                                                                                                                                                                                                                                                       PKVKLOSNGPVAKKAKKETSSSDSSEDSSEEDKAQVPTQKAAAPAKRASLPQHAGKAAA 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   877 CKSASAHNLSSE-----KKTGHPRTSMLQKSLSVIASAKEKTLGLAGKTQTAGVEE 927
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSINSAWSEHSLDPEDIRDELKKLYAQLEIYKRKKMITNNPHLQKKRCSKKGLGRSIMRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            758 ITEIPETVSRQCSKEDKEGADHGTAKGTALIRKNPPESSGNTGKSKEETLKNRVFSLKKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 -DEAPOT------OKPKAAATAAKAPTKAQTKAPAKPGPPAKAQPKAANGKAGSSSSS
                                                                                                                                                                                                                                          Indels 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1157 SSNNFQQPLTSRAEVCPWEFETPAQPNAGRSVALPASSALSANKIAGPRKEE 1208
                                                                                                                                                                                  Length 734;
                                                                                                                                                                           Score 190.5; DB 2;
Pred. No. 0.0062;
                                                                                                                                                                                                                                       239;
                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                     665 PKFSHSSNNP-----RDDIATEAYED---ELDMGR--
                                                                                                                                                                                                                                    92;
                                                                                                                                                                           7. Match 3.0%;
Local Similarity 21.3%;
nes 126; Conservative 95
                                                                                                                                                                                                              Best Local Sir
Matches 126;
                                                                                                                                                                              Query Match
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nucleolus-cytoplasm shuttle phosphoprotein N;Alternate names: Noppl40 protein B C;Species: Rattus norvegicus (Norway rat)

RESULT 10 B42680

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A;Reference number: A86625; MUID:21235186; PMID:11337471
A;Accession: A86827
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1072 <STO>
A;Cross-references: GB:AE005176; PID:912724625; PIDN:AAK05715.1; GSPDB:GN00146
A;Experimental source: strain IL1403
A;Genetics:
A;Genetics:
A;Genetics:
                                                                                                                                                                                                                                                                              32;
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T29776
hypothetical protein C50F2.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-oct-1999 #sequence_revision 15-oct-1999
C;Accession: T29776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SDLNPGTTQMKDNFDIGEVC---PWEVYDLTPGP--VPSESKVQKHVSIVASEMEKNPTF 1042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1043 SLKEKSHHKPKAAEVCQQSNQKRIDKAEVCLWESQGQSILEDEKLLISKTPVLPERAKEE 1102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1103 NGGQPRAANVCA-----GQSEELPPKAVASKTENENLNQIGHQEKKTSSSEENVRGSYN 1156
                                                                                                                                                                                                                                                                                                                                                      ----AWSEHSLDPEDIRDELKKL---YAQLEIYKRKKMITNNPHLQKKRCSKKGLGRSIM 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMSSNBESEHSNSSNI-NETNNSSEITNILPPSNPTESNSVSDQTSSEASTNSNSSI-S 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----VIASAKEKTLGLAGKTQTA------GVEERTKSQKPL------PKDKETN 942
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    943 RNHSNSDN-----TETKDPAPQNSNPAEEPRKPQKSGIMKQQRVN-----PTTAN 987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              632 SNSMSSINSPSLSLSLTSNSESATNQSNSSEATKVDNNSSTHSSNILNSGSNDSSDSDS 691
                                                                                                                                                                                                                                                                                                                          --TVTIGLLL 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSPSNISSTSDSESATNSSDFSNVAEVANNSLASVNNSSSSVLSSTSTADNLGINQSGSD 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        572 VANNSLASVNNSSSSVLSSTSTADNLEINQFGSDNLTKDSSEISTSGAFLSSNQTSSEAS 631
                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              664 I-----PKFSHSSNNPRDDIATEAYEDELDMGRSGSYLNSSINS------
                                                                                                                                                                                                                                                                                                                                                                                                                                             RRITEIPETVSRQCSKEDKEGA-----DHGTAKGTALIRKNPPESSGNTGK-SKEETLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NRVFSLKKS-HSTYDHVRDQTEESSSL-----PTE-----SQEEETTENSTLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIS-----SPISTISSSQQK----ESQSNLLNTIEGI---NNPITFNNSSSE
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                                                                                                                                                                                                                                                                              Indels 254;
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                                                                                                                                                                                                                                  Length 1072;
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                                                                                                                                                                                                                               Score 188; DB 2;
Pred. No. 0.014;
                                                                                                                                                                                                                                                                                                                          618 HNELIISAIFHTIRFVLASRLQSDWMLMLYFAHTHLTV----
                                                                                                                                                                                                                                                    Similarity 18.9%; Pred. No. 0.01.46; Conservative 109; Mismatches
                                                                                                                                                                                                                                  2.9%;
18.9%;
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                                                                                                                                                                                                                                                                              Matches 146;
                                                                                                                                                                                                                                  Query Match
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R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
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                                                                                                                                                                                                                                                                            for normal growth and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20;
                                                                                                                                                                                                                                                                                                                                                                                              .Cross-references: EMBL:AB009080; NID:d1228566; PID:d1034109; PIDN:BAA33143.1
                                                                                                                                Cispecies: Dictyostellum discoideum)
Cispecies: Dictyostellum discoideum)
Cispecies: Dictyostellum discoideum
Cispecies: Dictyostellum discoideum
Cispecies: Dictyostellum discoideum
Cispecies: Dictyostellum discoideum
Risaito, J.; Adachi, H.; Sutoh, K.
J. Biol. Chem. 273, 24654-24659, 1998
A;Title: Dictyostellum TRFA homologous to yeast Ssn6 is required for normal A;Reference number: 217852; MUID:98406112; PMID:9733762
A;Accession: T14004
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1390 <SAI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               901 ISRFEHQNNRTSSPFENNSNNNNNNNNNNNNNNINYNNIGQRALSPQSSQHKDRREIILDE 960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DKEGADHGTAKGTALIRK----NPPESSGNTGKSKE---ETLKNRVFSLKKSHSTYDHVR 825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSSEKKTGHPRTSMLQKSLSVIASAKEKTLGLAGKTQTAGVEERTKSQKPLPKDKETNRN 944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.0%; Score 190; DB 2; Length 1390; Best Local Similarity 21.1%; Pred. No. 0.016; Matches 111; Conservative 81; Mismatches 228; Indels 106;
         ---TP-KPQAGKANGVPASQ----NGKAGKESEE
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SSEEEKKKPKSKA-
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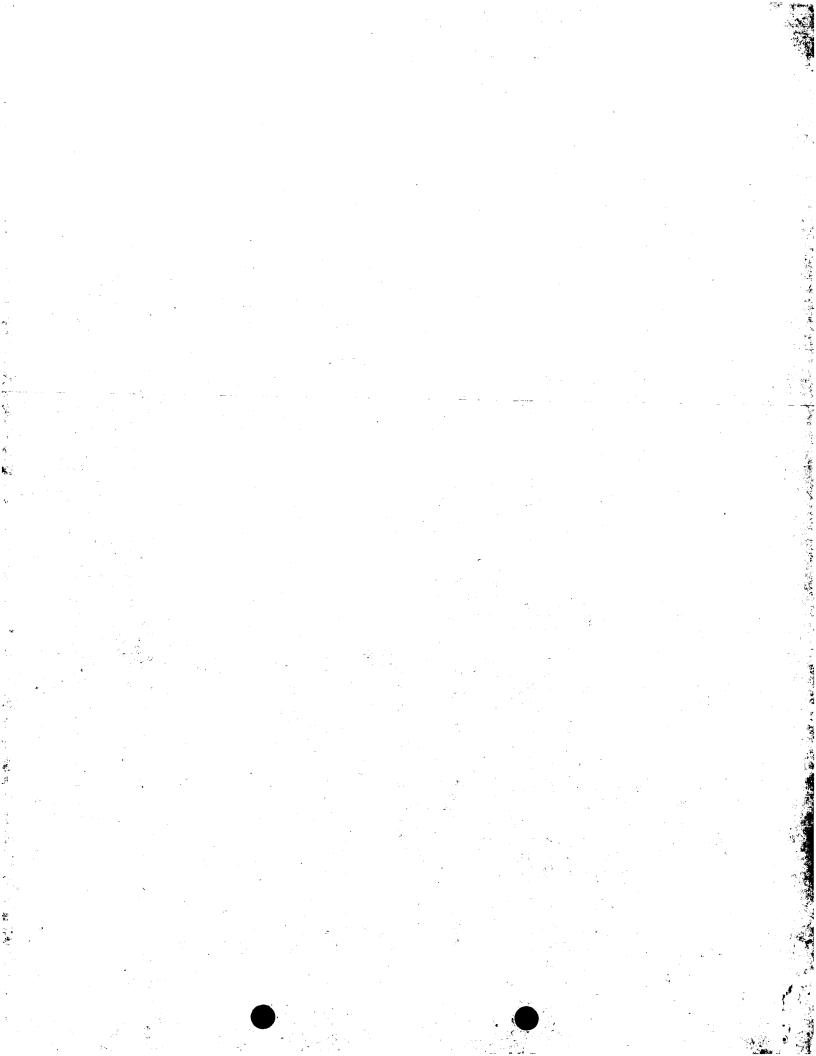
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Southwick, A.M.; Sun, H.; Tallo
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A:Introns: 34/3; 102/3; 163/2; 205/3; 269/3; 282/3; 564/3; 602/3; 622/2; 639/3; 667/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15;
                                                                                                                                                                                                                                                                                                                             GSPDB:GN00141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   709 LDP----EDIRDELKKLYAQLEIYKRKKMITNNPHLQKKRCSKKGLGRSIMRRITEIPET 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        765 VSRQ----CSKEDKEGADHG---TAKGTALIRKNPPESSGNTGKSKEETLKNRVFSLKKS 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 DKKKDGKMVSKKHEEG--HGDLEVKESDVKVEEHEKEHKKGKEKKHEELEEEKEGKKKKN 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138 KKEKDESGPEEKNKKADKEKKHEDVSQEKEELEEEDGKKNKKKEKDESGTEEKKKPKKE 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KSASAHNLSSEKKTGHPRTSMLQKSLSVIASAKEKTLGLAGKTQTAGVEERTKSQKPLPK 937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKETNRNHSNSDNTETKDPAPQNSNPAEEPRKPQKSGIMKQQRVNPTTANSDLNPGTTQM 997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235 HDETDQEMKEKDSKKNKKKEKDESCAEEKKKKPDKEKKEKDESTEKEDKKLKGKKGKGEK 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22 LDPKEKGENVEVEMEVKAKSIEKVKAKKDEESSGKSKKDKEKKK--GKNVDSEVKEDKDD 79
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A; Reference number: A86141; MUID:21016719; PMID:11130712 A; Accession: C96608 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-522 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             818 HSTYDHVRDQTEESSSLPTESQEEETTENSTLESLSGKKLTQKLKEDSEAESTESVPLVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEKEDEGK - - KTKEHDATEQEMDDEAADHKEGKKKKNKDKAKKKETVIDEVCEK - - - - ET
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A;Cross-references: EMBL:AL049607; GSPDB:GN00062; ATSP:F11C18.80
A;Experimental source: cultivar Columbia; BAC clone F11C18
                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE005173; NID:g9954748; PIDN:AAG09099.1; C;Genetics: A;Gene: F25P12.91 A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.9%; Score 186; DB 2; L 19.7%; Pred. No. 0.007; ative 90; Mismatches 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 96; Conserv
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           R;Du, Z.; Le, T.T.
submitted to the EMBL Data Library, November 1996
submitted to the EMBL Data Library, November 1996
A;Description: The sequence of C. elegans cosmid C50F2.
A;Reference number: 220684
A;Status: preliminary: translated from GB/EMBL/DDBJ
A;Nolecule type: DNA
A;Residues: 1-1046 < DDZ>
A;Cross-references: EMBL:U80445; PIDN:AAB37795.1; GSPDB:GN00019; CESP:C50F2.2
A;Cross-references: EMBL:U80445; PIDN:AAB37795.1; GSPDB:GN00019; CSP:C50F2.2
A;Genetics:
C;Genetics:
A;Genetics:
A;Map position: 1
A;Introns: 72/2; 888/1; 940/1; 986/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                995 TQMKDNFDIGEVCPWEVYDLTPGPVPSESKVQKHVSIVASEMEKNPTFSLKEKSHHKPKA 1054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1055 AEVCQQSNQKRIDKAEVCLWESQGQSILEDEKLLISKTPVLPERAKEENGGQPRAANVCA 1114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : : :| | ::| | ::| | 410 QPSQKPADLTPKPITLASKSPITRSSEVSTEPSTKPKRAPIVWDDKPKDSTA-KELPKEL 468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  254 -RSKIAKKAP------ISQRVQFPRMPAPQAPDAVASKVREQKPVDITPHPRP 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        354 PITPETLPSRNSEIOKPAA--SKIOEKKTEVIARSOKS--EASTKIAOKPSPINPTVNFK 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------RTSMLQKSLSVIASAKEKTLGLAGKTQTAGVEERTK-SQKPLPKDKETNRN 944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   945 HSNSDNTE-----TKDPAPQNSNPAEEP-RKPQKSGIMKQQRVNPTTANSDLNPGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.9%; Score 187; DB 2; Length 1046;
22.3%; Pred. No. 0.016;
tive 86; Mismatches 220; Indels 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 22.3
Matches 122; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----SQGQSILEDEKLLISKTPVLPERAKEENGGQPRAANVCAGQSEELPPKAVA---- 1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1127 --SKTENENLNQIGHQEKKTSSSEENVRGSYNSSNNFQQPLTSRAEVCPWEFETPAQPNA 1184
                                                                                                      735 TNNPH---LQKKRCSKKGLGRSIMRRITEIPETVSRQCSKED--KEGADHGTAKGTALIR 789
                                                                                                                                                                                                                                    790 KNPPESSGNTGKSKEETLKNRVFSLKKSHSTYDHVRDQTEESSSLPTESQEEETTENSTL 849
                                                                                                                                                                                                                                                                ESLSGKKLTQKLKEDSEAESTESVPLVCKSASAHNLSSEKKTGHPRTSMLQKSLSVIASA 909
                                                                                                                                                                                                                                                                                                                                           910 KEKTLGLAGKTQTAGVEERTKSQKPLPKDKETNRNHSNSDNTETK----DPAPQNSNPAE 965
                                                                                                                                                                                                                                                                                                                                                                                                                     634 AKKKHLVIYDDGDQEILYLKNQKWSPLDESELSQDEEAADQTGQEEDASTVGSGAGSSKA 693
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              747 SRSKKDISSVSKSG-KSKASSKKKEEPSKATTSSKSKSGPVKS------VPAKSKT 795
Ouery Match 2.9%; Score 183; DB 2; Length 852;
Best Local Similarity 19.6%; Pred. No. 0.02;
Matches 121; Conservative 92; Mismatches 211; Indels 192; Gaps
                                                                            680 TEAYEDELDMGRSG----SYLNSSINSAWSEHSLDPEDIRDELKKLYAQLEIYKRKKMI 734
                                                                                                                                                                                              338 -DNPRNTDLNNTTEEKPDVEHQIEEKENESSSVKQADLSKDSDIKEETEPAELLDSKDVL 396
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796 GKGKAKSGSASTPASK 811
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completed: February 15, 2003, 08:32:03 ne : 57.8197 secs rch co time



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OM protein - protein search, using sw model

February 15, 2003, 04:22:33 ; Search time 18.7541 Seconds
(without alignments)
2687.074 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-775-181-2 6382 1 MGAMAYPLLCLLLAQLGLG......LSANKIAGPRKEEIWDSFKV 1215

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

112892

imum DB seq length: 0 aximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	3385 ra	P31424 rattus norv	canis f	P41777 rattus norv	homod	homo	drosc	P11978 saccharomyc	staph		homod	bos t		mus m	P35601 mus musculu	P12036 homo sapien	tetra	Q28820 oryctolagus		014340 schizosacch	Q9u7e0 caenorhabdi	рошо	homo	caenc	P43597 saccharomyc	P29374 homo sapien	haemo		P53278 saccharomyc	P06102 saccharomyc	P46100 homo sapien		m
SUMMARIES	ID	MGR1_RAT	MGR5_RAT	TRDN_CANFA	NP14_RAT	MGR5_HUMAN	MGR1_HUMAN	MGR_DROME	SIR4_YEAST	MRSP_STAAU	TRDN_HUMAN	ANK2_HUMAN	CYL1_BOVIN	TPR_HUMAN	CASR_MOUSE	AC15_MOUSE	NFH_HUMAN	MLH_TETTH	TRDN_RABIT	CASR_RAT	YB35_SCHPO	ATRX_CAEEL	CYL1_HUMAN	NFM_HUMAN	MGR1_CAEEL	YFI6_YEAST	RBB1_HUMAN	IGA4_HAEIN	TCOF_HUMAN	YG3A_YEAST	NOT3_YEAST	ATRX_HUMAN		TRP_DROME
	Length DB	1199	1203 1			1212 1			1358 1	1637 1	728 1	3924 1	667 1	2349 1	1079 1	1131 1	1020 1	633 1	705 1	1079 1	1310 1	1359 1		•		1233 1			1411 1			2492 1	952 1	1275 1
œ	Query Match Length	δ.	•			٠	•		•	•	•	•	•				•		•	•	•	•		٠		•	•	•	•			•	5.6	
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	Result No.	1	7	m	4	ß	9	7	σο	σ,	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

P18583 homo sapien P06180 xenopus lae Q6688 mus musculu Q14832 homo sapien O84419 chlamydia t P46012 caenorhabdi P70486 rattus norv Q02552 homo sapien Q4493 homo sapien	P98193 rattus norv P30414 homo sapien
SON_HUMAN HIBN_XENLA HTRX_MOUSE MGR3_HUMAN PWPC_CHLTR RXTS_CABEL ATRX_RAT MGR3_RAT MGR3_RAT MGR3_RAT MGR3_RAT TGN2_HUMAN	DMP1_RAT
2426 589 2476 877 1770 952 527 879 1781	489 1462
	2.5
165 164.5 163.5 163.5 162.5 162 162	161
8888884444 40078801128	44

## ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- MISCELLANEOUS: ACTIVATED BY QUISQUALATE > GLUTAMATE > IBOTENATE
                               TRANS-1- AMINOCYCLOPENTYL-1,3-DICARBOXYLATE; INHIBITED BY 2-AMINO- 3-PHOSPHONOPROPIONATE. SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro: IPR001828; ANF_receptor.
InterPro: IPR000337; GPCR_Mgr.
Pfam; PF01094; ANF_receptor; 1.
Pfam; PF01094; ANF_receptor; 1.
PRINTS; PR00248; GPCRMGR.
PROSITE; PS00999; G_PROTEIN_RECEP_F3_1; 1.
PROSITE; PS00981; G_PROTEIN_RECEP_F3_2; 1.
PROSITE; PS50259; G_PROTEIN_RECEP_F3_2; 1.
PROSITE; PS50259; G_PROTEIN_RECEP_F3_3; 1.
PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
G_PROTEIN COUPLED G_PROTEIN COUPLED G_PROTEIN G_PRO
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N-LINKED (GLCNAC. ..) (POTENTIAL).
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MW; EEESA04C50694B9F CRC64;
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CYTOPLASMIC (POTENTIAL).
VI (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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8; Pred. No. 0.00057;
120; Mismatches 330;
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18.6%;
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PIR; A41939; A41939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----ERFKLLQEFVYEREGNTEEDELEEEEDLPTASKLTPEDSPALTPPSPFRDS 1159
439 YHFRKAKSIRASGLILLETILFGSLLLYFPVVILYFEPSTFRCILLRWARLLGFATVYGT 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSNSDNTETKDPAPQNSNPAEEPRKPQKSGIMKQQRVNPTTANSDL------NPGTTQ 996
                                                                                                                                                             545 TSSVCQNLEKQISLIGQGKTSDHLIFNMCLIDRWDYMTAVA-EFLFLLWGVYLCYAVRTV 603
                                                                                                                                                                                       PSAFHEPRYMAVAVHNELIISAIFHTIRFVLASRLQSDWMLMLYFAHTHLTVTVTIGLLL 663
                                                                                                                                                                                                                                                                IPK----FSHSSNNPRDDIATEAYEDELDMG------RSGSYLNSSINSAWSEHSLDP 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                 --IFRRKKPGAGNANSNGKSVSWSEPGGRQAPKGQHVWQRLSVHVKT 919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         765 VSRQCSKEDKEGADHGTAKGTALIRKNPPESSGNTGKSKEETLKNRVFSLKKSHSTYDHV 824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RDQTEESSSLPTESQEEETTENSTLESLSGKKLTQKLKEDSEAESTESVPLVCKSASAHN 884
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       885 LSSEKKTGHPRTSMLQKSLSVIASAKEKTLGLAGKTQTAGVEERTKSQKPLPKDKETNRN 944
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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Brain;
MEDLINE-92317054; PubMed-1320017;
Abe T., Sugihara H., Nawa H., Shigemoto R., Mizuno N., Nakanishi S.;
"Molecular characterization of a novel metabotropic glutamate
                                                                                                         : | :|: ::
LVTKTNRIARILAGSKKKICTRKPRFMSAWAQVIIASILISVQLTLVVTLII------
                                     615 VLYRDTPVVKSSSRELCYIILAGIFLGYVCPFTLIAKPTTTSCYLQRLLVGLSSAMCYSA
                                                                                --FLSRTAQRIPYMTGGRVMRMLAVILLVVFWFLIGW
                                                                                                                                                                                                                                                                                                                                                                                                           EDIRDELKKLYAQLEIYKRKKMITNNPHLQKKRCS-----KKGLGRSIMRRITEIPET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   832 TPKMYIIIAKPERNVRSAFTT --- SDVVRMHVGDGKLPCRSNTFLN -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Metabotropic glutamate receptor 5 precursor (mGluR5).
GRM5 OR GPRCIE OR MGLUR5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VCAGQSEELPP--KAVASKTENENLNQIGHQEKKTSSS 1147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VASGSSVPSSPVSESVLCTPPNVTYASVILRDYKQSSS 1197
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P31424;
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1095 IPKEIQLPTTMTTFAE----IQPLPAIEVT----GGAQGATGVSPAQETPTGAESAPGK 1145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IECFTPKGSMGNGGRATMSSSNGKSVTWAQNEKSTRGQHLWQRLSVHINKKENPNQTAVI 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OCSKEDKEGADHGTAKG------TALIRKNPPESSGNTGKSKEETLKNRVF 812
                                                                                     219 ETEWFHGLRRKWRPHLHRRGPNOGPRGLGHSWR-----RKDGLGGDKSHFKWSPPYLECE 273
                                                                                                                    DVKWFDDYYLKLRPETNLRNP-----WFQEFWQHRFQCRLEGFAQENSKYNKT-----CN 381
                                                                                                                                                          --MKVDINLQ 311
                                                                                                                                                                                           SSLTLRTHHVQDSKMGFVINAIYSMAYGLHNMQMSLCPGYAGLCDAMKPIDGRKLLDSLM 441
                                                                                                                                                                                                                                                                                                                      FINTITCIIMLAFVPIYF-----GSNYKIITMCFSVSLSATVALGCMFVPKVYIILAKP
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                                                                                                                                                                                                                             KVDIDQCSSDGWFSGTHKCHLNNSECMPIKGLGFVLGAYECICKAGFYHPGVLPV----
                                                                                                                                                                                                                                                              KTNFTGVSGDM1LFDENGDSPGRYE1MNFKEMG---KDYFDY1NVGSWDNGELKMDDDEV
                                                                                                                                                                                                                                                                                                                                                                    DD-SPCFVQEDKYLR----LAIISFQGLCMLLDFVSMLVVYHFRKAKSIRASGLILLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    615 VAVHNELIISAIFHTIRFVLASRLQSDWMLMLYFAHTHLTVTVTIGLLLIPK----FSHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                         457 TILFGSLLLYFPVVILYFEPSTFRCILLRWARLLGFATVYGTVTLKLHRVLKV----
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                                                    248;
                  Score 211; DB 1; Length 1203; Pred. No. 0.0017;
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                                                                                                                                                          --SYKPGWLV-TLSSAIYGL---QPNLVPEFRGV-
                                                    Conservative 128; Mismatches 400;
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                                    Similarity
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ID TRDN_CANFA
                                                    Matches 179;
                  Query Match
                                      Best Local
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                                                                                                              Minakami R., Katsuki F., Sugiyama H.;
Minakami R., Katsuki F., Sugiyama H.;
"A variant of metabotropic glutamate receptor subtype 5: an
evolutionally conserved insertion with no termination codon.";
Biochem. Biophys. Res. Commun. 194:622-627(1993).
-!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-
CALCIUM SECOND MESSENGER SYSTEM AND GENERATES A CALCIUM-ACTIVATED
                                                                                                                                                                                                                                                         SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; 5A (SHOWN HERE) AND 5B; ARE
PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER BY AN INSERTION OF
                                                                                                                                                                                                                                                                                                                            -!- TISSUE SPECIFICITY: WIDELY DISTRIBUTED IN NEURONAL CELLS OF THE CENTRAL NERVOUS SYSTEM.
-!- MISCELLANEOUS: ACTIVATED BY QUISQUALATE > GLUTAMATE > IBOTENATE TRANS-1- AMINOCYCLOPENTYL-1, 3-DICARBOXYLATE.
-!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS. STRONGEST, TO MGLURI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLCNAC. .) (POTENTIAL).
) (GLCNAC. .) (POTENTIAL).
) (GLCNAC. .) (POTENTIAL).
(IN ISOFORM SA).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001828; ANF_receptor.
InterPro; IPR001828; ANF_receptor.
InterPro; IPR001837; GPCR_Mgr.
Pfam; PF01094; ANF_receptor; 1.
Pran; PF01094; GPCRMGR.
PROSITE; PS00979; G_RROTEIN_RECEP_F3_1; 1.
PROSITE; PS00999; G_PROTEIN_RECEP_F3_2; 1.
PROSITE; PS00999; G_PROTEIN_RECEP_F3_2; 1.
PROSITE; PS00999; G_PROTEIN_RECEP_F3_3; 1.
PROSITE; PS00259; G_PROTEIN_RECEP_F3_3; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal; Maltigene family; Alternative_Splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC...) (POTEN MISSING (IN ISOFORM 5A).
receptor mGluR5 coupled to inositol phosphate/Ca2+ signal
                                                                   SEQUENCE OF 859-923 FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
VII (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                Biol. Chem. 267:13361-13368(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D10891; -; NOT_ANNOTATED_CDS
EMBL; S64315; AAB27666.1; -.
                                                                                     TISSUE=Brain;
MEDLINE=93343913; PubMed=7688218;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28;
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EEKVVKQVKATEKAAIEKTVKPKPAKKAEHQEKESPTIKTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KPKPTSKETPEVTES -> GILQVVPVVLNCLFLVQFQQDE
ELNVESKVFRMIHVLSHPTSRTSPILVISTTCRT (IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  642 WMLMLYFAHTHLTVTVTI-GLLLIPKFSHSS-----NNPRDDIATEAYEDELD-MGRSGS 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                          Biol. Chem. 274:28660-28668(1999).
- FUNCTION: MAY BE INVOLVED IN ANCHORING CALSEQUESTRIN TO THE JUNCTIONAL SARCOPLASMIC RETICULUM AND ALLOWING ITS FUNCTIONAL COUPLING WITH THE RYANDDINE RECEPTOR (BY SIMILARITY).
- SUBCELLULAR LOCATION: Type II membrane protein. Sarcoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 695 YLNSSINSAWSEHSLDPEDIRD------ELKKLYAQLEIYKRKMITNNPH---
                                                                                                                                                                                                                                                                                 ALTERNATIVE PRODUCTS: 3 ISOFORMS; CARDIAC ISOFORM 1, SKELETAL
                                                                                    Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKQIQ (IN CARDIAC ISOFORM 1).
MISSING (IN CARDIAC ISOFORM 1).
E -> EPIKGKEVKVPGSLKEKE (IN CARDIAC
                                                                                                                              SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
TISSUB-Heart, and Skeletal muscle;
MEDLINE-99428545; Pubmed-10497235;
Kobayashi Y.M., Jones L.R.;
"Identification of triadin 1 as the predominant triadin isoform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. .) (POTENTIAL)
DOYAFCRYMIDMFVHGDLRPG -> GKHSEEVAGG
                                                                                                                                                                                                                                                                                             ISOFORM (SHOWN HERE) AND CARDIAC ISOFORM 3; ARE PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.2%; Score 201.5; DB 1; Length 700; 22.3%; Pred. No. 0.0027; tive 98; Mismatches 252; Indels 135;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC (POTENTIAL).
                                                                     Canis familiaris (Dog).
Eukaryota, Metazoa: Chordata; Craniata; Vertebrata;
Mammalia: Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transmembrane; Sarcoplasmic reticulum; Glycoprotein;
                                                                                                                                                                                                                                                                                                                    -!- TISSUE SPECIFICITY: SKELETAL AND CARDIAC MUSCLE.
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N-LINKED (GLCNAC. ..)
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                       Last sequence update)
Last annotation update)
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                                                                                                                                                                                              expressed in mammalian myocardium.
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            Created)
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AAF00223.1;
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          15-JUN-2002 (Rel. 41,
15-JUN-2002 (Rel. 41,
15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alternative splicing
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MEDILNE=20143579; Pubmed=10679015;
A Yang Y., Isaac C., Wang C., Dragon F., Pogacic V., Meier U.T.;
Tonserved composition of mammalian box H/AcA and box C/D small
nucleolar ribonucleoprotein particles and their interaction with the
common factor Nopp40.";
Mol. Biol. Cell 11:567-577(2000).

- FUNCTION: RELATED TO NUCLEDCOGENESIS, MAY PLAY A ROLE IN THE
MAINTENANCE OF THE FUNDAMENTAL STRUCTURE OF THE FIBRILLAR CENTER
C AND DENSE FIBRILLAR COMPONENT IN THE NUCLEDLOS. IT HAS INTRINSIC
C GTPASE AND ATPASE ACTIVITIES. MAY PLAY AN IMPORTANT ROLE IN
TRANSCRIPTION CATALYZED BY RNA POLYMERASE I (BY SIMILARITY).
C GTPASE AND ATPASE ACTIVITIES. MAY PLAY AN IMPORTANT ROLE IN
TRANSCRIPTION CATALYZED BY RNA POLYMERASE I (BY SIMILARITY).
C -!- SUBGNIT: Interacts with DKc1/Nap57, Nop5/Nap65 and fibrillarin.
C -!- SUBGNIT: THEFACKS EXPEND FROM THE DEBNSE
C -!- SUBCELLULAR LOCATION THESE TRACKS EXPEND FROM THE DEBNSE
EIBRILLAR COMPONENT OF THE NUCLEDLUS ACROSS THE NUCLEOPLASM TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1100 KEENGGQPRAANVCAGQ----SEELP-----PKAVASKTENENLNQIGH-QEKKTSSS 1147
                                                                                                                                                                                                                                     PPLPTVQASRPTPASPTLE---GKEEEEKKKAEKKVTSETKKKEKEKEDVKKKSDKDTAIDV 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   400 KSSKKEHSAPSEKQVKAKTERAKEETSAASTKKAVP--GKKEEKTTKTVEQEIRKEKSGK 457
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                         227 AKVKEVQKTPPKAKEKEGKETAAVAKH---EQKDQYAFCRYMIDMFVHGDLRPGQSPALP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 458 TSTASKDKEP---EIKKD----EKMPKADKEVKPKPPQSQVKKEEKSESQVKKEAKPEQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           511 IAKPEKTVSHGKPEEKVVKQ-------VKATEKAAIEKT-VKPKPA
                                                                                                                                                                         -SLPTESQEEETTENSTLESLSGKKLTQKLKED----SEAESTESVPLVCKSASAHNLSS
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Nucleolar phosphoprotein pl30 (Nucleolar 130 kDa protein) (140 nucleolar phosphoprotein) (Noppl40) (Nucleolar and coiled-body
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Meier U.T., Blobel G., "Nopp140 shuttles on tracks between nucleolus and cytoplasm.";
L----IRKNPPESSGNTGKSKEETLKNRVFSLKKSHSTYDHVRDQTEESS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND SEQUENCE OF 292-309 AND 563-601
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INTERACTION WITH NOP5 AND FIBRILLARIN.
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609 KESLQ-SHNVTKAEKPARVSREDL 631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NSDLNPGTTQMKDNFDIGEVCPWEVYDLTPGPVPSESKVQKHVSIVASEMEKNPTFSLKE 1046
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                                                                                                                                                                                                    PTM: THIS PROFEIN UNDERGOES RAPID AND MASSIVE PHOSPHORYLATION AND DEPHOSPHORYLATION ON CK-II AND PKC SITES. NOPP140 IS ONE OF THE MOST PHOSPHORYLATED PROFEINS IN THE CELL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92; Mismatches 240; Indels 134; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 704;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 199; DB 1;
Pred. No. 0.0036;
LIMITED NUMBER OF NUCLEAR PORE COMPLEXES
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Matches 126; Conservative
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704 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93343913; PubMed=7688218;
Minakami R., Katsuki F., Sugiyama H.;
Minakami R., Katsuki F., Sugiyama H.;
M variant of metabotropic glutamate receptor subtype 5: an
evolutionally conserved insertion with no termination codon.";
Biochem. Biophys. Res. Commun. 194:622-627(1993).
-!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
MEDIATED BY A G-PROTEIN THAY ACTIVATES A PHOSPHATIDYLINOSITOL.
CALCIUM SECOND MESSENGER SYSTEM AND GENERATES A CALCIUM-ACTIVATED
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SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; 5A (SHOWN HERE) AND 5B; ARE PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER BY AN INSERTION 32 RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Minakami R., Katsuki F., Yamamoto T., Nakamura K., Sugiyama H.;
Molecular cloning and the functional expression of two isoforms
human metabotropic glutamate receptor subtype 5.";
Biochem. Biophys. Res. Commun. 199:11136-1143 (1994).
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PRINTS; PR00248; GPCRMGR.
PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
PROSITE; PS00981; G_PROTEIN_RECEP_F3_2; 1.
PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal; Multigene family; Alternative splicing.
   SSNNFQQPLTSRAEVCPWEFETPAQPNAGRSVALPASSALSANKIAGPRKEE 1208
                                     REVISIONS. .
Katsuki F.,;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Metabotropic glutamate receptor 5 precursor (mGluR5).
                                                                                                                                                                                                                                      ΑA
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InterPro, IPR000337; GPCR_Mgr.
Pfam; PF00003; 7tm_3; 1.
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MEDLINE-94197696; PubMed=7908515;
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MGR2_HUMAN

ID MGR2_HUMAN

AC P41594,

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SEQUENCE FROM N.A.
MEDLINE=96029774; PubMed=7476890;
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                                 TPKG-----SMGNGGRA-
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Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL.
- CALCIUM SECOND MESSENGER SYSTEM. MAY PARTICIPATE IN THE CENTRAL
ACTION OF GLUTAMATE IN THE CNS, SUCH AS LONG-TERM POTENTIATION IN
THE HIPPOCAMPUS AND LONG-TERM DEPRESSION IN THE CEREBELLUM.
-!- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVGATGGAGCAGAGPGGPESPDAG--PKALYDVAEAEEHFPAPA-------RPRSPS 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |----STLSHRAGSASRTDDDVPSLHSEPVARSSSQGS-LMEQISSVVTRFTANISE 1074
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LNPGTTQMKDNFDIGEVCPWEVYDLTPG---PVPSESKVQKHVSIVASEMEKNPTFSLKE 1046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KSHHKPKAAEVCQQSNQKRIDKAEVCLWESQGQSILEDEKLLISKTPVLPERAKEENGG- 1105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QPAAGAQAAGDAARESPAAGPEAAAKPDLEELVAL-----TPPSPFRDSVDSGST- 1178
                                                                                                                                                                                                                                                 887 SEKKTG------HPRTSMLQKSLSVIASAKEKTLGLAGKTQTAGVEERTKSQK 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLPKDKETNRNHSNSDNTETKDPAPQ-NSNPAEEPRKPQKSGIMKQ--QRVNPTTAN-SD 989
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"Cloning and expression of a human metabotropic glutamate receptor 1
alpha: enhanced coupling on co-transfection with a glutamate
TAKGTALIRKNPPESSGNTGKSKEETLKNRVFSLKKSHSTYDHVRDQTEESSSLPTESQE
                                                                                        ----TMSSSNGKSVTWAON
                                                                                                                                                                                      EETTENSTLESLSGKKLTOKL----KEDSE----AESTESVPLVCKSASAHNLS
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MEDLINE-97231349; Pubmed-9076744;
Stephan D., Bon C., Holzwarth J.A., Galvan M., Pruss R.M.;
"Human metabotropic glutamate receptor 1: mRNA distribution,
chromosome localization and functional expression of two splice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1162 QQPLTSRAEVCPWEFETPAQPNAGRSVALPAS 1193
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992 -PGTTQMKDNFDIGEVCPWEVYDLTPGPVPSE--SKVQKHVSIVASEMEKNPTFSLKEKS 1048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1057 GPGN------GLRSLYPPPPPPQHLQMLPLQLSTFGEELVSPPADDDDDSE 1101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            882 AHNLSSEKKTGHPRTSMLQKSLSVIASAKEKTLGLAGKTQTAGVEERTKSQKPLPKDKET 941
                                                                                                                                                                                                                                                                                           RTVPSAFHEPRYMAVAVHNELIISAIFHTIRFVLASRLQSDWMLMLYFAHTHLTVTVTIG 660
                                                                                                                                                                                                                                                                                                                                                                     661 LLLIPK----FSHSSNNPRDDIATEAYEDELDMG-----RSGSYLNSSINSAWSEHS 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  762 PETVSRQCSKEDKEGADHGTAKGTALIRKNPPESSGNTGKSKEETLKNRVFSLKKSHSTY 821
   -----CPFC-----ADDSPCFVQEDKYLR-----LAIISFQGLCMLLDFVSMLVV 438
                                                                       439 YHFRKAKSIRASGLILLETILFGSLLLYFPVVILYFEPSTFRCILLRWARLLGFATVYGT 498
                                                                                                                                               --FLSRTAQRIPYMTGGRVMRMLAVILLVVFWFLIGW 544
                                                                                                                                                                                                                   545 TSSVCQNLEKQISLIGQGKTSDHLIFNMCLIDRWDYMTAVAEF----LFLLWGVYLCYAV 600
                                                                                                                                                                                                                                                   -----MEPPMPIL-----SYPSIKEVYLICNTSNLGVVAPLGYNGLLIMSCTYYAFKT 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DHVRDQTEESSSLPTESQEEETTENSTLESLSGKKLTQKLKEDSEAESTESVPLVCKSAS 881
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P91685; Q9V485;
15-JUL-1998 (Fel. 41, Last sequence update)
15-JUL-1908 (Rel. 41, Last sequence update)
15-JUL-2002 (Rel. 41, Last annotation update)
15-JUL-2002 (Rel. 41, Last annotation update)
MGtabotropic glutamate receptor precursor.
GLU-RA OR GLURA OR GLUI144.
Drosophila melanogaster (Fruit fly).
Enkaryota: Metazoa: Arthropoda: Mandibulata: Pancrustacea: Hexapoda:
Insecta; Perygota: Neoptera: Endopterygota: Diptera: Brachycera:
MUSCOMORPHA: Ephydroidea: Drosophiliae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       978 VHRRVPSAATTPPLPPHL-----TAEETPLFLA-------EPALPKG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------IFRRKKAGAGNANSNGKSVSWSEPGGGQVPKGQHMWHRLSVH
                                                                                                                                                                                                                                                                                                                  709 LDPEDIRDELKKLYAQLEIYKRKKMITNNPHLQKKRCS-----KKGLGRSIMRRITEI
                                   555 YVQDEFTCKACDLGWWPNADLTGCEPIPVRYLEWSNIEPIIAIAFSCLGILVTLFVTLIF
                                                                                              : | : |: | | | | | |: 675 LVTKTNRIARILAGSKKKICTRKPRFMSAWAQVIIASILISVQLTLVVTLII------
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                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license greement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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N-LINKED (GLCNAC. . .) (POTENTIAL).
NOWER (SUNSERGGOVIPKG -> KKRQPEFSPSSQCPSAH VQL (IN ISOFORM BETA).
MISSING (IN ISOFORM BETA).
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           ARE PRODUCED BY ALTERNATIVE SPLICING.
SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
STRONGEST, TO MGLURS.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA (SHOWN HERE) AND BETA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METABOTROPIC GLUTAMATE RECEPTOR 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.0%; Score 193; DB 1; Length 1194;
18.7%; Pred. No. 0.014;
ive 114; Mismatches 326; Indels 276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE, PS00979; G_PROTEIN_RECEP_F3_1; 1.
PROSITE, PS00980; G_PROTEIN_RECEP_F3_2; 1.
PROSITE, PS00981; G_PROTEIN_RECEP_F3_3; 1.
PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Multigene family; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLUIAR (POTENTIAL).
I (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
II (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
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P -> S (IN REF. 3).
W; 970E51AF40584F40 CRC64;
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CYTOPLASMIC (POTENTIAL).
IV (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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ASP/GLU-RICH (ACIDIC).
SER-RICH.
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                                                                                                                                                                                                                                                                                                        EMBL, AL096867; CAB75694.1; -- EMBL, AL035698; CAB65991.1; -- EMBL, AL035698; CAB65992.1; -- Genew, HGNC:4593; GRM1.
                                                                                                                                                                                                                                                                    L76627; AAB05337.1; -. L76631; AAB05338.1; -.
                                                                                                                                                                                                                                                       U31216; AAA87844.1; -.
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1194 AA; 132376
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Matches 165;
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                                                                                                                                                                           RA Adams A.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
George R.A. Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Worthan J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazes F.G., Change M., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Baytrakracyolu L., Beasley E.M.,
Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chadra I.,
RA Burtis K.C., Busam D.A., Dahlke C., Davenport L.B., Davies P.,
Burtis K.C., Busam D.A., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Burtis M.L., Evangelista C.C., Ferraz C., Ferriara S., Fleischmann W.,
RA Boson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F. Gorrell J.H., Wei M. Glasser K.,
A Glodek A., Gong F. Gorrell J.H., Wei M. H.H., Ibegwam C.,
Jalli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.
Jalli M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.
Jalli M., Malush R.N., Nixon K., Nuszon D.M., Nelson D.L.,
Merkulov G., Milshina N.V., Li J., Li Z., Liang Y., Lin Z.,
And Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Ra Bazzolo M., Pittumo G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Ra Barzolo M., Pittumo G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Shiert K., Wassarman D.A., Weinschen E., Wang A.H., Wang Z.-Y., Wassarman D.A., Weinschen B.C., Siden K.A., Woodege T., Woolly K.C., Shugoon M., Stung G., Zhao Q., Zhao Q., Zhao Q., Zhao Q., Zhao Q., Zhao G., Zha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- FUNCTION: RECEPTOR FOR GLUTAMATE.
-- SUBCELULAR LOCATION: Integral membrane protein.
--- DEVELOPMENTAL STAGE: EXPRESSED IN THE CNS OF THE LATE EMBRYO.
--- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
                                     Parmentier M.L., Pin J.P., Bockaert J., Grau Y.; "Cloning and functional expression of a Drosophila metabotropic glutamate receptor expressed in the embryonic CNS."; J. Neurosci. 16:6687-6694(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00003; 7tm_3; 1....3.
Pfam; PF00004; AME_receptor; 1.
PROSTTE; PS000948; GPCRMGR.
PROSITE; PS00999; G_PROTEIN_RECEP_F3_1; 1.
PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
                                                                                                                                                   STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001828; ANF_receptor.
InterPro; IPR000337; GPCR_Mgr.
                   MEDLINE=96421661; PubMed=8824309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE003846; AAF59402.1; -
FlyBase; FBgn0019985; Glu-RA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X99675; CAA67993.1; -.
                                                                                                                                 SEQUENCE FROM N.A.
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SREQNLQDDLDWYQALVW----SLLEGEPSISRAAITFSTDS-LSAPAPQVFLQATREES 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----IYGLQPNLVPEFRGVMKVDI-NL 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            311 QKVDIDQCSSDG-----WFSGTHKCHLNNSECMPIKGLGFVLGAYECICKAGFYHPG 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----IKKQQGDTCCWICDSCESFEYVYDEFTCKDCGPGLWPYADKLSCYALDIQYMKW 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----LAIISFQGLCMLLDFVSMLVVYHFRK---AKSIRASGLILLETILFGSLLLY 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOVVITTSLIAIOVLITMIWMVVEPPGTRFYYPDRR-EVILKCKIODMSFLFSOLYNMIL 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  215; Indels 168; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 295 AKRANLSQPFHWIASDGWGKQQKLLEGLEDIAEGAITVELQSEIIADFDRYMMQLTPETN 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R------ILLQDLSSSAPHLANATLETEWFHGLRRKWRPHLHRRGPNQGPRG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           400 CDDSYRLSEKVGYEQESKTQFVVDAVYAFAYALHNLHNDRCNTQSDQTTETRKHLQSESV 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  363 VLPVNNFRRRGPDQHI----SGSTKDVSEEAYVCLPCREGCPFCADDSPCFVQEDKYLR- 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FPVVILYFEPSTFRCILLRWARLLGFATVYGTVTLKLHRVLKVF--LSRTAQRIPYMTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  246 LGHSWRRKDGLGGD---KSHFKWSPPY-----------------LECENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R----VMRMLAV-ILLVVFWFLIGWTSSVCQNLEKQISLIGQGKTSD-----HLIFNMCL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  355 ORNPWFAEYWEDTFNCVLTSLSVK-PDTSNSANSTDNKIGVKAKTE------
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ransmembrane; Glycoprotein; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                  IV (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                 II (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
III (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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VII (POTENTIAL).
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N-LINKED (GLCNAC...) (FN-LINKED (GLCNAC...)
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CYTOPLASMIC (POTENTIAL).
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N-LINKED (GLCNAC. . .)
V -> A (IN REF. 1).
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Pred. No. 0.036;
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Matches 119; Conservative
        coupled
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TRANSMEM
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DOMAIN
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1199-1205 AND 1217-1224.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria;
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                                                                  308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22;
                                                                                                                                                                                                                                                                                                                                                                      STRAIN-S288C / AB972;
Murphy L., Harris D., Barrell B.G., Rajandream M.A.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THE PROTEINS SIR1 THROUGH SIR4 CONTROL THE EXPRESSION OF
MATING TYPE GENES RESIDENT AT LOC1 OF EITHER END OF CHROMOSOME
III. SIR3 AND SIR4 ASSOCIATE WITH THE C-TERMINUS OF RAP1 TO FORM A
DNA-BINDING COMPLEX THAT INITIATES THE REPRESSION AT THE HM LOCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P--LKKGSADIGASVISLTKDKSIRKDTVEEK--KEEKLNIGKNFAHSDSL--SVPKVSA 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----AWSEHSLDPEDIRDELKKLYAQLEIYKRKKMITNNPHLQK 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         743 KRCSKKG---LGRSIMRRITE---IPETVSRQCSKEDKEGADHGTAKGTALIRKNPPESS 796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          648 FAHTHLTVTVTIGLLLIPKFSHS----SNNPRDDIATE-AYEDELDMGRSGSYLNSSIN 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transcription regulation; Repressor; DNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKPVRTIVPISTSQTNNSFLSGVKSLLSEEKIRDYSKEILG-----INLANEQPVLEK
                                                                                                                                                                                                       Marshall M., Mahoney D., Rose A., Hicks J.B., Broach J.R.; "Functional domains of SIR4, a gene required for position effect regulation in Saccharomyces cerevisiae."; Mol. Cell. Biol. 7:4441-4452(1987).
                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.8%; Score 181; DB 1; Length 1358; 20.8%; Pred. No. 0.069; 1ve 78; Mismatches 233; Indels 15:
                                                                             Regulatory protein SIR4 (Silent information regulator 4). SIR4 OR STE9 OR ASD1 OR UTH2 OR YDR227W OR YD9934.12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 P -> L.
152061 MW; 9C698765964F094E CRC64;
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                                                                                                                                                                                                                                                                                        MEDLINE-95192063; PubMed=7885847; Davies C.J., Hutchison C.A. III; Insertion site specificity of the transposon Tn3."; Nucleic Acids Res. 23:507-514(1995).
                                                                                                                                       Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                    01-OCT-1989 (Rel. 12, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT: INTERACTS WITH RAP1 C-TERMINUS
             1358 AA
             PRT;
                                                                                                                                                                                           MEDLINE=88142836; PubMed=3325825;
                                       01-OCT-1989 (Rel. 12, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U13239; AAC33144.1; -. EMBL; Z48612; CAA88507.1; -. PIR; A29360; A29360.
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             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1358 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S0002635; SIR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND TELOMERES
                                                                                                                                                  NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Sim
Matches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coiled coil
           SIR4_YEAST
P11978;
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SIR4_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1012 YDLTPGPVPSESKVQKHVSIVASEMEKNPTFSLKEKSHHKPKAAEVCQQSNQKRIDKAEV 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLWESQGQSILEDEKLLISKTP----VLPERAKEENGGQPRAANVCAGQ---SEELP 1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---DPAPQNSNPAEEPRKPQKSGIMKQQRVNPTTANSDLNPGTTQMKDNFDIGEVCPWEV 1011
                                                                                                                                                                                             ---KLDENS-ANSTVASALDTNGTSATTETLTSKKIVPSPKKVAIDQ---DKITLHDEKTL 361
                                                                                                                                                                                                                                                                                                                                               - LQKVQGESHIDSRNNTLNVTPSKRPQLGEIPNPMKKHKPNEGRTPNISNCTINIQKKLE 553
GNTGKSKEETLKNRVFSLKKSHSTYDHVRDQTEESSSLPTESQEEETTENSTLESLSGKK 856
                                                                                                                                                                                                                                                                                                    --PKDKETNRNHSNSDNTETK-- 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein of Staphylococcus aureus.";
Eur. J. Bacchem. 236:904-910(1996).
-!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SYRAIN=Isolate 1061;
Savolaten K., Kuusela P., Paulin L., Korhonen T.K.;
"Pls, a large repeat-rich surface protein of methicillin resistant
                                                                                                                                                  857 LTQKLKEDSEAESTESVPLVCK--SASAHNLSSEKKTGHPRTSMLQKSLSVIASAKEKTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421 FLVEYEGQENNYNSTSRSTEKKNDMNTSAKNKNGENKKIG-------------
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BDDLINE=96270743; PubMed=8665912;
Hilden P., Savolainen K., Tyynelae J., Vuento M., Kuusela P.;
"Purification and characterisation of a plasmin-sensitive surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 676-682; 938-948; 1156-1168; 1176-1185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PKAVASKTENENLNQIGHQEKKTSSSEENVRGSYNSSNNFQQPLTSR 1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillales; Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Methicillin-resistant surface protein precursor.
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TIGREAMS; TIGR01167; LPXTG_anchor; 1.
TIGREAMS; TIGR01168; YSIRK_signal; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001899; Gram_pos_anchor
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P80544; Q9ZF62;
01-FEB-1996 (Rel. 33, Created)
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                                                                                                                                                                                                                                                                                                    915 GLAGKTQTAGVEERTKSQKPL---
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Dest Local Similarity
Matches 139; Conserv
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INIT_MET 0
DOMAIN 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     1091 KTPVLPERAKEENGGOPRAANVCAGQSEELPPKAVASKTENENLNOIGHQEKKTSSSEEN 1150
                                                                                                                                                                                                                                                                                                                                                            972 KSGIMKQQRVNPTTANSDLNPGTTQMKDNFDIGEVCPWEVYDLTPGPVPSESKVQKHVSI 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Denborough M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular cloning of the cDNA encoding human skeletal muscle triadin and its localisation to chromosome 6q22-6q23.";
Eur. J. Blochem. 233:258-265(1995).
-!- FUNCTION: MAY BE INVOLVED IN ANCHORING CALSEQUESTRIN TO THE JUNCTIONAL SARCOPLASHIC RETICCULUM AND ALLOWING ITS FUNCTIONAL COUPLING WITH THE RYANODINE RECEPTOR (BY SIMILARITY).
                                                                                                                                                                                                                                   :| ||::|:
VTKDTTEQASTEEKANTTEQASTEEKADTTEQATTEEAPKAEGTDKVETEEAPKAEETDK 150
                                                                                                                                                                                                                                                                                                                             204 SKAATEEAPKAEETEKTATEEAPKTEETDKVETEEAPKAEETSKAATEKAPKAEETNKVE 263
                                                                                                                                                                                                                                                                                                                                                                                                                              309 VAKDLYKKSEVTEAEKAEIEKVLPKDISNLSNE--------EIKKIALS 349
                                                                                                                                                                                                                                                                  ESTESVPLVCKSASAHNLSSEKKTGHPRTSMLQKSLSVIASAKEKT-----LGLAGKT 920
                                                                                                                                                                                                                                                                                                               921 QTAGVEERTKSQ-----KPLPKDKETNRNHSNS--DNTETKDPAPQNSNPAEEPRKPQ 971
                                                                                                                                                                         ETVSRQCSKEDKEGADHGTAKGTALIRKNPPESSGNTGKSKEETLKNRVFSLKKSHSTYD 822
          Glycoprotein; Cell wall; Peptidoglycan-anchor;
                                                                                                                                                                                                                       HVRDQTEESSS------EDSEETTENSTLESLSGKKLTQKLK-----EDSEA 867
                                                                                                                                                                                               EAAENNTTQKQDDSSDASKVKGNV---QTIEQSSAN---SNESDIPEQV-----D 90
                                                      REMOVED BY SORTASE (POTENTIAL).
141 X 2 AA TANDEM REPEATS OF D-[SAG].
LPXTG SORTING SIGNAL (POTENTIAL).
MAIDE-LINKED TO CELL WALL (POTENTIAL).
MW. 75BE9ADB469BD309 CRC64;
                                            METHICILLIN-RESISTANT SURFACE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 264 TEEAPAAEETNKAATEETPAVEDTNAKSN------SNAQPSETERTQVVDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1151 VRGSYNSSNNFQQPLTSRAEVCPWE----FETPAQPNAGRSVALPASSALSANK 1200
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                                                                                                                                                  71; Mismatches 197; Indels 108;
                                                                                                                          Length 1637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Skeletal muscle;
MEDLINE-96061957; PubMed-7588753;
Taske N.L., Eyre H.J., O'Brien R.O., Sutherland G.R.,
Foster P.S.
                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                       0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                728 AA
                                                                                                                           Score 178;
                                                                                                                                       Pred. No.
GRAM_POS_ANCHORING;
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                                                                                                     AA; 174573
                                                                                                                                                  Conservative
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1601
1637
1582
1602
            resistance;
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(Rel. 39,
(Rel. 39,
                                                                                                                                     l Similarity
99; Conserv
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PROSITE; PS50847;
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1602
1301
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                        Repeat; Signal
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Triadin.
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30-MAY-2000
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Q13061;
            Antibiotic
                                                                                          MOD_RES
SEQUENCE
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DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          642 WMLMLYFAHTHLTVTVTI-GLLLIPKFSHSS-----NNPRDDIATEAYEDELDMGRSGSY 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LNSSINSAWSEHSLDPEDIRDE-----LKKLYAQLEIYKRK------KMITNNPH 739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           389 EOPKGKKOEKKEKHVE-----PAKSPKKEHSVPSDKOVKAKTERAKEEIGAV 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             436 SSKKAVPGKKEEKTIKTVEQEIRKEKSGKTSSILKDKEPIKGKEEKVPASLKEKEPETKK 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------LPTESQEEETTENSTLESGKKLTQKLKEDSEAESTESVPLVC 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --PKDKETNRNHSNSDNTETKDPAPQNSNPAEEPRKPQKSGIMKQQRVNPTTANSDLN-- 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             277 VHGDLKPGQSPAIPPPLPTEQASRPTPASPALEEKEGEKKAEKKVTSETKKKEKEDIKK
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SUBCELLULAR LOCATION: Type II membrane protein. Sarcoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.8%; Score 177.5; DB 1; Length 728; 20.3%; Pred. No. 0.047;
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C1C53BBE1B2A0815 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              291;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LUMENAL.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                         : reticulum; Glyc
BY SIMILARITY.
CYTOPLASMIC.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                  EMBL; U18985; AAA75315.1; -. Genew; HGNC:12261; TRDN.
                                                                                                                                                                                                                                                                                                                                                                                                               Sarcoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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46
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RESULT 11 ANK2\_HUMAN

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REVISIONS.

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691 RSGSYL--NSSINSAWSEHSL------727
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(IN ISOFORM 2).
MISSING (IN ISOFORM 2 AND ISOFORM 3).
GQ -> PE (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 230; Indels 139;
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QY -> HA (IN REF. 1).
I -> Y (IN REF. 1).
WW; 52AC496C428E29D2 CRC64;
                                                                                                                                                                                 Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
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REPEAT A.
REPEAT A. (APPROXIMATE).
REPEAT A.
REPEAT A.
REPEAT A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 177.5; I
Pred. No. 0.4;
                   InterPro; IPR002110; ANK.
InterPro; IPR002110; ANK.
InterPro; IPR000906; Zu5.
InterPro; IPR00031; Zu5.
Pfam; PF00023; ank; 24.
Pfam; PF00731; death; 1.
Pfam; PF00731; Zu5; 1.
PRINTS; PR001415; ANKYRIN.
SMART; SM00248; ANK; 21.
SMART; SM00248; Zu5; 1.
PROSITE; PS50088; ANK_REPERAT; 20.
PROSITE; PS50097; ANK_REPERGION; 1.
PROSITE; PS50017; DEATH_DOMAIN; 1.
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  Genew; HGNC:493; ANK2.
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            106410;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chan W., Kordeli E., Bennett V.; "440-kD ankyrinB: structure of the major developmentally regulated domain and selective localization in unmyelinated axons."; J. Cell Biol. 123:1463-1473(1993).
                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-92009921; PubMed-1833308; Tre W.T., Menninger J.C., Yang-Feng T.L., Francke U., Sahr K.E., Lux S.E., Ward D.C., Forget B.G.; "Isolation and chromosomal localization of a novel nonerythroid
                                                                                                                                                                                                              TISSUE-Brain stem;
MEDLINE-91302466; PubMed-1830053;
OLTO E., Kunimoto M., McLaughlin T., Bennett V.;
Isolation and characterization of cDNAs encoding human brain ankyrins reveal a family of alternatively spliced genes.";
J. Cell Biol. 114:241-253(1991).
                                                                  001484; 001485;
01-APR-1993 (Rel. 25, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Ankyrin 2 (Brain ankyrin) (Ankyrin B) (Ankyrin, nonerythroid).
                                                                                                                                                                                                                                                                                                              Carpenter S.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AND FUNCTION (POTENTIAL).
SIMILARITY: CONTAINS 23 ANK REPEATS.
SIMILARITY: CONTAINS 1 DEATH DOMAIN.
662 DVPASKKAKEGTEDVSPTKQKSPISF 687
                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-94075409; PubMed-8253844;
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X56957; CAA40278.1; -. EMBL; X56958; CAA40279.2; -. EMBL; Z26634; CAB4264.1; -. EMBL; M37123; AAA62828.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 463-495 FROM N.A
                                                           STANDARD;
                                                                                                                                          Homo sapiens (Human)
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A39643; A39643.
B39643; B39643.
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S14569; S14569
; P42771; IDC2.
                                                                                                                                                                                                                                                                                                                                                             stem;
                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ankyrin gene.
                                                                                                                                                                                                                                                                                                                                                             TISSUE=Brain
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26;

Gaps

PIR; A PIR; B PIR; S HSSP; 1

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                                                                                                                                                                                                                                                                                                                                                                              1652 DETQSTQKQHKPSL--GIKKP---VRRKLKEKQ----KQKEEGLQASAEKAELKKGSSEE 1702
                                                                                                                                                                                                                                                                                                RVNP---TTANSDLNPGTTQMKDNFDIGEVCPWEVYDLTPG-----PVPSESKVQKHV 1029
                                  1592 IKGKVEKDSTGLVNYLTDDLNTCVPLPKEQLQTVQDKAGKKCEALAVGRSSEKEGKDIPP 1651
                                                                                                                                                                        1703 SLGEDPGLAPEPLPTVKATSPLIEETPIGSIKDKVKALOKRVED-EQKGRSKLPIRVKGK 1761
                                                                                                                                                                                                                                 1076 --SQGQSILEDEKLLISKTPVLPERAKEENGGQPRAANVCAGQSEELPPKAVASKTENEN 1133
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                                                                                                                                         879
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 -----YKRKKMITNNP----HLQK-----KRCSKKGLGRSIMRRITEIPE 763
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                    764 TVSRQCSKEDKEGADHGTAKGTALIRKNPPESSGNTGKSKEETLKNRV--FSLKKSHSTY
                                                                                                                                      822 DHVRDQTEESSSLPTESQEEETTENSTLESLSGK-KLTQKLKEDSEAESTESVPLVCKS-
                                                                                                                                                                                                           -----ASAHNLSSEKKTGHPRTSMLQKSLSVIASAKEK---TLGLAGKTO--
                                                                                                                                                                                                                                                                            -TAGVEERTKSQKPLPKDKETNRNHSNSDNTETKDPAPQNSNPAEEPRKPQKSG-IMKQQ
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01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1997 (Rel. 35, Last annotation update)
Cylicin I (Multiple-band polypeptide I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    667 AA
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MEDLINE=93359502; PubMed=8354692;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228 KYSKSSKNNSDAVSETCSKNSSNVGLM-VHLGES------DAESMEFDWMLKNYSQ 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLPKDKETNRNHSNSDNTETKDPAPQNSNPAEEPRKPQKSGIMKQQRVNPTTANSDLNPG 993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                   protein; Repeat; Sperm; Spermatogenesis.
9 APPROXIMATE TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180; Indels 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 667;
                                                                                                                                                                                                                                                                                                                                                                                                      74817 MW; CBF66EA462243D91 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.2%; Score 177; DB 1; 20.2%; Pred. No. 0.045;
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Nucleoprotein TPR.
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(Rel. 34, Last sequ
                    EMBL; 222779; CAA80456.1;
PIR; S35913; S35913.
PIR; A40713; A40713.
                                                                                                   Structural
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DOMAIN 28
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                                                                                                                                                                                                                                                                                                                                                                                 PUNCTION: COMPONENT OF THE CYTOPLASMIC FIBRILS OF THE NUCLEAR PORE COMPLEX IMPLICATED IN NUCLEAR PROTEIN IMPORT. ITS AMINO TERMINUS IS INVOLVED IN ACTIVATION OF ONOGENIC KINASES.
SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF THE NUCLEAR PORE COMPLEX. THE ASSEMBLY OF THE NPC IS A STEBWISE PROCESS IN WHICH TRP-CONTAINING PERIPHERAL STRUCTURES ASSEMBLE AFTER OTHER
                                                                                                           REVISIONS, AND CHARACTERIZATION.
MEDLINE=95096166; PubMed=7798308;
Byrd D.A., Sweet D.J., Pante N., Konstantinov K.N., Guán T.,
Saphire A.C.S., Mitchell P.J., Cooper C.S., Aebi U., Gerace L.;
"Tpr, a large coiled coil protein whose amino terminus is involved in activation of oncogenic kinases, is localized to the cytoplasmic surface of the nuclear pore complex.";
J. Cell Biol. 127:1515-1526(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPONENTS, INCLUDING P62.

TISSUE SPECIFICITY: HIGHEST IN TESTIS, LUNG, THYMUS, SPLEEN AND BRAIN, LOWER LEVELS IN HEART, LIVER, AND KIDNEY.

DISEASE: INVOLVED IN TUMORIGENIC REARRANGEMENTS WITH THE MET, TRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSLDPEDIRDELKKLYAQLEIYKRKKMITNNPH-----LQKKRCSKKGLGRSIMRRI 758
                  Mitchell P.J., Cooper C.S.; The human tpr gene encodes a protein of 2094 amino acids that has "The human tpr gene encodes a protein of 2004 amino acids that has extensive colled-coil regions and an acidic C-terminal domain."; Oncogene 7:2329-2333(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99; Mismatches 239; Indels 134;
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                                                                                                                                                                                                                                                                                                                               King H.W.S., Tempest P.R., Merrifield K.R., Rance A.J.;
"tpr homologues activate met and raf.";
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MEDLINE-93064711; PubMed-1437155;
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PIR, S00928, S00928.
Genew, HGNC:12017; TPR.
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SEQUENCE Query Match Local

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                                                                                                      1481 ETLNQAETKSKSLESQVENLQKTLSEKETEARNLQEQTVQLQSELSRLRQDLQDRTTQE- 1539
                                                                                                                                                                                                      ------EQLRQQITE--KEEKTRKAIVAAKSKIAHLAGVKDQLTKENEELKQRNGALD 1589
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090Y96; 008968; 088519; 090X95; 090Z08; 09R1D6; Q9R1X2;
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 41, Last sequence update)
Extracellular calcium-sensing receptor precursor (CaSR) (Parathyroid Call calcium-sensing receptor).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The calcium sensing receptor and its alternatively spliced form in murine epidermal differentiation.";
                                                     ---NTGKSKEETLKNRVFSLKKSHSTYD----HVRDQT----EESSSLPTESQEEETTEN
                                                                                                                                                           STLESLSGKKLTQKLKEDSEAESTESVPLVCKSASAH-----NLSSEKKTGHPRTSMLQ
                                                                                                                                                                                                                                                            901 K---SLSV-IASAKEKTLGLAGKT-----QTAGVEERTKSQKPLPKDKETNRN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi;
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STRAIN-C57BL/6; TISSUE-Kidney;
MEDLINE-20092890; Pubmed=10625662;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D., Koemueves L., Mauro T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM A), AND TISSUE SPECIFICITY STRAIN-Black Swiss X 129/SVJ; TISSUE=Kidney; MEDLINE-20119279; Pubmed=10652312;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  novel cation-sensing mechanism.";
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Elias P.M., Bikle D.D.;
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MEDLINE=20043955; PubMed=10579354;
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735 TNNPHLQKK----RCSKK---GLG----
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Matches 143;
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Chang W., Tu C., Chen T.-H., Komuves L., Oda Y., Pratt S.A., Miller S., Shoback D.; "Expression and signal transduction of calcium-sensing receptors in cartilage and bone."; Endocrinology 140:5883-5893(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR CALCIUM-SENSING RECEPTOR. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                 SEQUENCE OF 646-799 FROM N.A., AND TISSUE SPECIFICITY.

BEDILNE-9723187, Pubmed-90076582;

Quarles L.D., Hartle J.E. II, Siddhanti S.R., Guo R., Hinson T.K.;

"A distinct cation-sensing mechanism in MC3T3-E1 osteoblasts

"Inctionally related to the calcium receptor.";

J. Bone Miner. Res. 12:393-402(1997).

-i. FUNCTION: SENSES CHANGES IN THE EXTRACELLULAR CONCENTRATION OF

CALCIUM IONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A

G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND

MESSENGER SYSTEM.
                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE
PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: EPIDERMIS, KIDNEY AND CARTILAGE.
SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00003; 7tm_3; 1.
Pfam; PF01094; ANF_receptor; 1.
PRINTS; PR00249; GPCRMGT.
PROSITE; PS00999; G_PROTEIN_RECEP_F3_1; 1.
PROSITE; PS00981; G_PROTEIN_RECEP_F3_2; 1.
PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
PROSITE; PS00981; G_PROTEIN_RECEP_F3_4; 1.
G_protein coupled receptor; Transmembrane; Glycoprotein; Signal;
                                                                                    STRAIN=NMRI, TISSUE=Brain;
Hildenbrand J., Ammon H.P.T., Wahl M.A.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                             Moawad T.I., Riccardi D.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
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EXTRACELLULAR (POTENTIAL)
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II (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
VI (POTENTIAL).
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                                                                        SEQUENCE OF 507-582 FROM N.A. (ISOFORM A)
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InterPro; IPR000337; GPCR_Mgr.
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                                                                                                                                     SEQUENCE OF 562-814 FROM N.A.
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MGD; MGI:1351351;
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Moawad T.I., R
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889 LRRPNISRKRSSSLGGSTGSNPSSSISSKSNSEDRFPQPERQKQQQPLALTQQEQQQQPL 948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -GSTKDVSEE----AYVCLPCREG------CPFCADD-----SPCFVQEDKYLR 417
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P (IN REF. 3).
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MEDLINE=90229765; PubMed=1691767;
MEDLINE=90229765; PubMed=1691767;
MEDLINE=90229765. PubMed=1691767;
MEDLINE=90229765; PubMed=1691767;
MEDLINE=90229765; PubMed=1691767;
Mediation of inter and intramolecular primary structure homologies of interferons by a Monte Carlo method.";
J. Interferons Res. 10:31-31(1990).
-!-FUNCTION: THE ELOWGATION OF PRIMED DNA TEMPLATES BY DNA POLYMERASE DELTA AND EPSILON REQUIRES THE ACTION OF THE ACCESSORY PROTEINS FORM AND ACTIVATOR 1. THE 140 SUBUNIT BINDS TO THE PRIMER-TEMPLATE JUNCTION.
"Differentiation-specific element binding protein (DSEB) binds to a defined element in the promoter of the angiotensinogen gene required for the irreversible induction of gene expression during differentiation of 3T3-L1 adipoblasts to adipocytes.";
                                                                                                                                                                                                                              01-JUN-1994 (Rel. 29, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
140-OCT 1 140 kDa subunit (Replication factor C large subunit) (Al 140 kDa subunit) (Arctivator 1 large subunit)
(Al-1145) (Differentiation specific element binding protein)
RFCI OR RECCI OR IBF-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: HETEROPENTAMER OF SUBUNITS OF 140/145, 40, 38, 37, AND 36.5 kDa THAT FORMS A COMPLEX WITH PCNA IN THE PRESENCE OF ATP.
                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                    1009 NRHQALLPLQCAEADSEMTIQETGLQGPWYGDHQPEI-----ESPDEMSPALVVSTSRS
                                                        766 SR-----QCSKEDKEGADHGTAKGTALIRKNPPESSGNTGKSKEETLKNRVFSLKKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lossie A.C., Haugen B.H., Wood W.M., Camper S.A., Gordon
Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases
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MEDLINE-95388065; PubMed-7659092;
McGehee Habener J.F.;
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MEDLINE=94089669; PubMed=8265586;
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or send an email to license@lsb-sib.ch).
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                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration
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PROSITE; PS50172; BRCT; 1.
DNA replication; ATP-binding; Transcription regulation; DNA-binding;
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NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
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           SIMILARITY: BELONGS TO THE ACTIVATOR 1 140 KDA SUBUNIT FAMILY. SIMILARITY: CONTAINS 1 BRCT DOMAIN.
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E -> EPDPCLSCLIFFGIQ (IN REF. 4. V -> A (IN REF. 5).
N -> S (IN REF. 4).
MISSING (IN REF. 3 AND 4).
T -> A (IN REF. 1).
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3.6%; Pred. No. 0.12;
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 SUBCELLULAR LOCATION: Nuclear.
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EMBL; X72711; CAA51260.1; -.
EMBL; U36441; AAA7698.1; -.
EMBL; U07157; AAC52140.1; -.
EMBL; U15037; AAB60452.1; -.
MGD; MGI:97891; Recc1.
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Search completed: February 15, 2003, 08:27:12 Job time : 41.7541 secs

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- protein search, using sw model OM protein

February 15, 2003, 04:37:08; Search time 67.6488 Seconds (without alignments) 3700.688 Million cell updates/sec Run on:

US-09-775-181-2 6382 1 MGANAYPLLICLILAQLGLG......LSANKIAGPRKEEIWDSFKV 1215 Title: Perfect score:

Sequence:

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671580 Total number of hits satisfying chosen parameters:

671580 segs, 206047115 residues

Searched:

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTREMBL\_21:\*

1: Sp\_archea:\*
2: Sp\_bacteria:\*
3: Sp\_fungi:\*
4: Sp\_human:\*
5: Sp\_invertebrate:\*
6: Sp\_mammal:\* sp\_vertebrate:\*
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## SUMMARIES

Description	Ogult3 homo sapien	Ogakt3 macaca fasc	09vr40 drosophila	045500 caenorhabdi	Q9vka3 drosophila	Q9w1p3 drosophila	Q9y133 drosophila	Q9bml6 drosophila	Q9w1p4 drosophila	098uc4 gallus gall	Q9bml5 drosophila	Q9vps7 drosophila	Q8sy55 drosophila		Q9epv6 mus musculu	Q98uc5 gallus gall
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Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from macaque brain cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PQNSNPAEEPRKPQKSGIMKQQRVNPTTANSDLNPGTTQMKDNFDIGEVCPWEVYDLTPG 1017
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                                                                                                                                                                  PPESSGNTGKSKEETLKNRVFSLKKSHSTYDHVRDQTEESSSLPTESQEEETTENSTLES 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                               KTLGLAGKTQTAGVEERTKSQKPLPKDKETNRNHSNSDNTETKDPAPQNSNPAEEPRKPQ
                      LSGKKLTQKLKEDSEAESTESVPLVCKSASAHNLSSEKKTGHPRTSMLQKSLSVIASAKE
                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
101-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Hypothetical 34.7 kba protein.
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Macharyota Medata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1532.5; DB 6; Length
Pred. No. 2.1e-90;
3; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AB052146; BAB19001.1; -.
Hypothetical protein.
SEQUENCE 317 AA; 34746 MW; 26C0DB80505EFCC4 CRC64;
                                                                                                                                                                                                                                                                                                                                                              317 AA
                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ttch 24.0%; sal Similarity 93.4%; 297; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE-CEREBELLUM CORTEX;
                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                  1212 SFKV 1215
                                                                                                                                                                                                                                                                                                        541 SFKV 544
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121
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Hostins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M. Henderson S.N.,
Sutton G.G., Worthard J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Bardon R.C., Rogers Y.-H.C., Blazej R.G., Change M., Miklos G.L.G.,
RA Ballew R.M., Doyle C., Baxter E.G., Helt G., Nolson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Cawley S., Dahlke C., Davenport L.B., Davies P., A
Burtis R.C., Busam D.A., Buller H., Cadlew E., Center A., Chadra I.,
RA Burtis R.C., Busam D.A., Dahlke C., Davenport L.B., Davies P., A
Burtis R.C., Busam D.A., Buller H., Cadlew E., Center A., Chadra I.,
RA Burtis R.C., Busam D.A., Buller H., Cadlew E., Center A., Chadra I.,
RA Burtis R.C., Gabrielian A.E., Davies P., Davies P.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Burtis N.C., Garg N.S., Garg N.S., Gelbart W.M., Glasser K.,
A Glodek A., Gong F., Gorrell J.H., Gu Z., Gennar P., Harris M.,
RA Hostin D., Houston K.A., Helman T.J., Hernandez J.R., Hetchum K.A.,
A Hostin D., Houston K.A., Helman T.J., Hernandez J.R., Retchum K.A.,
A Hostin D., Houston K.A., Molland T.J., Well M.-H., Ibegwan C.,
A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.
A Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
A Lasko P., Lei Y., Molland T.J., Hernandez J.R., Retchum K.A.
A Merkulov G., Milshina N.V., Mobarry C., Morris J., Woshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Murshy D., Lei S., Shan H.,
Relinert K., Renlington K., Saunders R., Venter E., Wang X.,
Wang Z.-Y., Wassarman D.A., Walontey K.C., Wu D., Yang S., Yao Q.A.,
Wang Z.-Y., Wassarman D.A., Walontey C.C., Scheeler F., Shang X.H., Zhong F.N., Zhong F.N., Shang A., Shang S., Shang S., Shang S., Shang S., Sheng X.H., Zh
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                             241 GHQEKKT-SFEENVRGSYNSSNNFQQPLMSRAEVCPWEFETPAQPNAGRSVALPVSSALS
                                                                                                               GHQEKKTSSSEENVRGSYNSSNNFQQPLTSRAEVCPWEFETPAQPNAGRSVALPASSALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00003; 7tm_3; 1. PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
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                                                                                                                                                                                                                                                              ANKIAGPRKEEIWDSFKV 1215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                300 ASKIAGPRKEEVWDTFKV 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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Q9VR40;
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Q9VR40
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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              218 NSICALI-CIALIPIVCYQRKRQHEARGWALMELFLIGASILYSVLFLDFVAPPEYGCCV 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104 DKSSFQQIPPFDVSFARRTHFYGLQLNCTGNNHR--WLPRL--VFVSHDPN---NSNKKA 156
                                                                                                                                                                                                                                                                                                                                                                                                       KVDINLQKVDIDQCSSDGWFSGTHKCHLNNSECMPIKGLGFVLGAYECICKAGFYHPGVL 364
                                                                                                                                                                                                                                                                                                                                                                                                                                           157 YLTLQLDQFDVDMCS---------AVNCHTKCTWTVHGGL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            424 QGLCMLLDFVSMLVVYHFRKAKSIRASGLILLETILFGSLLLYFPVVILYFEPSTFRCIL 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WTSSVCQNLEKQISLIGQGKTSDHLIFN----MCLIDRWDYMTAVAEFLFLLWGVYLCYA 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     439 VIIVAPKFYLSNGEPSRRSMTLG-----GHSGRAHPSLAKLRDNILNGTIDFAEVPIA 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLDPEDIRDELKKLYAQLEIYKRKKMITNNPHLQKKRCSKKGLGRS--IMRRITEIPETV 765
                                                                                                                                                                                                                                                                                                                             ----LECENGSYKPGWLVTLSSAIYGLQPNLVPEFRGVM 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           381 ARN--SDWLERWQFTVAVCLEAVITLMANLIRYSIRNSGRADTLFIVSFVHLQLTVSVNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RVS-----CNSDDVILCRTDAERGRHMLLAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     484 LRWARLLGFATVYGTVTLKLHRVLKVFLSRTAQRIPYMTGGRVMRMLAVILLVVFWFLIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLLLIPKFSHSSNNPRDDIATEAYEDELDMGRSG-----SYLNSSINSAWSE-H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVNNFRRRGPDQHISGSTKDVSEEAYVCLPCREGCPFCADDSPCFVQED-KYLRLAIISF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        600 VRIVPSAFHEPRYMAVAVHNELIISAIFHTIRFVLASRLQSDWMLMLYFAHTHLTVTVTI
                                                                                                                                                                                                                                                                                      Indels 131;
                                                                                                                                                                                                                                                  DB 5; Length 594;
                                         to the EMBL/GenBank/DDBJ databases
                                                                                                                               "Genome sequence of the nematode C.elegans: A platform investigating blology": Science 282:2012-2018(198). EMBL: Z92834: CABOT388.2: -SEQUENCE 594 AA: 67920 MW; 80AFIFC165AB9070 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                Score 408.5; DB 5;
Pred. No. 6.1e-18;
89; Mismatches 192;
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                                                                                             MEDLINE=99069613; PubMed=9851916,
                                                                                                                                                                                                                                                6.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                  Best Local Similarity 25.0 Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                             DKSHFKWSPPY -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                       Submitted (MAR-1997)
                                                           [2]
SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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CG17215.
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Q9VKA3
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                                                                           27;
                                                                                                             110 GKWPALASAHPSLHRALDTLTHATNFLNVMLQSNKSREQNLQDDLDWYQALVWSLLEGEP 169
                                                                                                                                                                                        SISRAAITFSTDSLSAPAPQVFLQATREESRILLQDLSSSAPHLA-----NATLETEWF 223
                                                                                                                                                                                                                                                                                                   HNKAYLGSYWRE------LGAAWNSTDGTQ-----EWGAPFRDCNLLTRRWL 139
                                                                                                                                                                                                                                                                                                                                                                                   187
                                                                                                                                                                                                                                                                                                                                                                                                                       394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CSKKGLGRSIMRRITEIPETVSRQCSKEDKEGADHGTAKG-----TALIRKNPPESSGN 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                6 GKWPC-RMFYDYTDIAEDAARQFIEFL----SGKFPNANTPIAID------EP 47
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NCBI_TaxID=6239;
                                                                                                                                                                                                                      48 --TRAEVSRRANGIAS------YALNEDDNLLAFAIAAPSIHTVVVKFRDNVTIPPDQV
                                                                                                                                                                                                                                                                                                                                                                           WPFRISFS-----EHR-IKVVAAAFIAADEDVC-NDGLEEVFGRRHGCDRNTTFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               358 VDFRTRKAHRW-VLRDVDLLKYLGTMVFAVICYMAAFTASSLDLLESAQLESLREADT--
                                                                                                                                                                                                                                                                  HG---LRRKWRPHLHRRGPNQGPRGLGHSWRRKDGLGGDKSHFKWSPPYLECENGSYKPG
                                                                                                                                                                                                                                                                                                                                           281 WLVTLSSAIYGLQPNLVPEFRGVMKVDINLQKVDIDQCSSDGW---FSGTHKCHLNNSEC
                                                                                                                                                                                                                                                                                                                                                                                                                     MPIKGL-GFVLGAYECICKAGFYHPGVLPVNNFRRRGPDQHISGSTKDVSE--EAYVCLP
                                                                                                                                                                                                                                                                                                                                                                                                                                             CREGCPFCADDSPC--FVQE-----DKYLRLAIISFQGLCMLLDFVSMLVVYHFRKAKSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CPGGCTNCDSNGVCLTFQEEEVLNVDACLRLLVAIVLGACILCCIVLGVIVFRQRKCKAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KVFLSRTAQRIPYMTGGRVMRMLAVILLVVFWFLIGWTSSVCQNLEK-QISLIGQGKTSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HLIFNMCLIDRWDYMTAVAEFLFLLWGVYLCYAVRTVPSAFHEPRYMAVAVHNELIISAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FYFLRFVYLPEMSPSAILLALFIRSOLTNSFALGLIFVPKLWYQHKQGTSHD----AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DELDMGRSGSYLNSSINSAWSEHSLDPEDIRDELKKLYAQLEIYKRKKMITNNPHLQKKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       123;
                                       699
                                       Length
                                                                           Indels
75242 MW; FFE5721445DAB5F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
               9.0%; Score 571.5; DB 5;
26.1%; Pred. No. 2.5e-28;
wiematches 316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA
                                                                         Conservative 113; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                       Matches 195;
SEQUENCE
                                     Query Match
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RA Adams M.D. Celnigers S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celnigers S.E., Holt R.A., Evans C.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champpe M., Pfeiffer B.D.,

RA Abril J.F., Agbayani A., Da Helt G., Nelson C.R., Miklos G.L.G.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Ballew R.M., Basu M., Butler H., Cadieu E., Center A., Chandra I.,

RA Burtis R.C., Buckam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Borkvaz D., Botchan M.R., Bouck J., Burtler P., Brottler P.,

RA Borkvaz D., Botchan M.R., Bouck J., Brotses P.,

RA Borkvaz D., Botchan M.R., Bouck J., Brotses P.,

RA Gorovaz D., Botchan M.R., Bouck J., Borkstein P., Brottler P.,

RA Borkvaz D., Botchan M.R., Bouck J., Borkstein P., Brottler P.,

RA Gorovaz D., Botchan M.R., Bouck J., Bourkes P.,

RA Gorovaz D., Botchan M.R., Garzel J., B., Davies P.,

RA Gorovaz D., Botchan M.S., Gebart W.M., Glasser K.,

Glodek A., Gong F., Gorrell J.H., Gu Z., Renizera S., Felsschman W.,

RA Harris N.L., Harvey D., Helman T.J., Wei M.-H., Ibegwam C.,

Allali M., Malush F., Karpen G.H., Re Z., Kennison J.A., Retchman B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Markulov G., Milshina N.V., Mobarry C., Morris J., Woshrefi A.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Santh T.,

RA Sher E., Stradling A.C., Stapleton M., Strong R., Santh T.,

RA Sher E., Stradling A.C., Stapleton M., Strong S., Yao Q., A.,

RA Sher E., Shradling A.C., Stapleton M., Strong S., Zhu X., Smith H.,

RA Sher E., Shradling A.C., Stapleton M., Strong S., Zhu X., Smith H.,

RA Sher E., Shradling A.C., Stapleton M., Strong S., Zhu X., Smith H.,

RA Sher S., Wolser E.W., Runin G.W., Wence S., Wall S., Shradly S., Shradly S., Shradly S., Shradly 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              443 KAKSIRASGLILLETILFGSLLLYFPVVILYFEPSTFRCILLRWARLLGFATVYGTVTLK 502
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tive 98; Mismatches 238; Indels 118;
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                               MEDLINE-20196006; PubMed-10731132;
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RAGAMRAINE-20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Endell M.D., Zhang O., Chen L.X.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Barndon R.C., Rogers Y.-H.C., Blazzl R.G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxter B.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Barllaw R.M., Basu A., Baxter B.P., Bhandari D., Bolshakov S.,
RA Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Berson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Gawley S., Dahlke C., Davenport L.B., Davies P.,
Anchry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Butler H., Cadieu E., Center A., Chandra I.,
RA Dockon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dockon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn R.A.
RA Dockon K., Doup L.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorell J.H., Gu Z., Guan P., Harris M.,
RA Jalali M., Kalush F., Karpen G.H., Kravitz S., Kulp D., Lai Z.,
Hasko P., Lei Y., Levitsky A.A., Li Z., Liang Y., Lin X.,
Munt S.M., Moy M., Murphy B., Murphy L., Morris J., Moshrefi A.,
Murt S.M., Moy M., Murphy B., Murphy L., Murzhy D.M., Nelson D.L.,
RA Ralazzolo M., Pittman G.S., Pan M., Sthen P., Shen H.,
RA Shien E.C., Siden-Kiamos I., Simpson M., Strong R., Sunth T.,
RA Shier E., Spradling A.C., Stapeler M., Strong R., Sunth T.,
RA Shies E., Spradling A.C., Stapeler B., Wang A.H., Wang Y.H.
1360 FKGQGDKWDQ------KAKVRSITASFSLNGVGLVPEESPDLYQENEELKEQVQKLAHQ 1412
                                                                                                                                                                        1510 SDEEEAALIAQFRRLFAPILDDS------LNLYYQLNDLDDTEHVRIHQTVAQ 1556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1557 MNDLTSSEEFTM-----ATQVNSPSPPPVGVELLLPISSDSST----ASSSLY 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LSVIASAKEKTLGLAGKTQTAGVEERTKSQKPLPKDKETNRNHSNSDNTETKDPAPQNSN 962
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                 LEIYKRKKMITNNPHLQKKRCSKKGLGRSIMRRITEIPETVSRQCSKEDKEGADHGTAKG
                                                                                                                                                                                                                                                                                               785 TALIRKNPPESSGNTGKSK--EETLKNRVFSLKKSHSTYDHVRDQTEESSSLPTESQEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   843 TTENSTLESLSGKKLTQKLKEDSEAESTESVPLVCKSASAHNLSSEKKTGHPRTSMLQKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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01-JUN-2001
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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Adams W.D., Celniker S.E., Holf W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Hichards S., Ashburner M., Henderson S.N.,
B. Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
R. Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelifer B.D.,
RA Man K.H., Doyle C., Baxer B.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
Ra Beson K.Y., Bencos P.V., Berman B.P., Bhandari D., Botchan M.S., Bouck J., Brokstein P., Brottier P.,
Ra Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Ra Borkova D., Botchan M.S., Boulk C., Davenport L.B., Davies P.,
Ra de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Rolet K.J., Evangeliste C.C., Ferraz C., Ferriera S., Fleischmann W.,
R. Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
A Harris N.L., Harrey D., Heinan T.J., Hernandez J. R., Houck J.,
R. Horett N.L., Harrey D., Heinan T.J., Hernandez J. R., Houck J.,
R. Hucett N.L., Harrey D., Heinan T.J., Hernandez J. R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
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Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
FINBL: AERO3461; AAR470131. -
FINBLS AFRO03461; AGR470131. -
FINBLS AFRO03461; GGR678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          472 LYFEPSTFRCILLRWARLLGFATVYGTVTLKLHRVLKVFLSRTAQRIPYMTGGRVMRMLA 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      532 VILLVVFWFLIGWTSSVCQNLEKQISL--IGQGKTSDHLIFNMCLIDRWDYMTAVAEFLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LLWGVYLCYAVRTVPSAFHEPRYMAVAVHNELIISAIFHTIRFVLASRLQSDWMLMLYFA
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                                                                                                                                                                                                                                                                                                                                                                                                                  Length 264;
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                                                                                                                                                                                                                                                                                                 PRINTS; PR00248; GPCRMGR.
PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
SEQUENCE 264 AA; 29532 MW; CAC5623C52703642 CRC64;
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01.NOV-1999 (TrEMBLrel. 12, Last sequence update)
01.NOV-1999 (TrEMBLrel. 20, Last annotation update)
BCDNa:GH07312 protein.
GABA-B-R2 OR BCDNA:GH07312 OR CG6706.
                                                                                                                                                                                                                                                                                                                                                                                                      4.4%; Score 281; DB 5;
28.5%; Pred. No. 2.9e-10;
:live 49; Mismatches 96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 28.5
nes 65; Conservative
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                                                                                                                                                                                                                                                                     Pfam; PF00003; 7tm_3; 1
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NCBI_TaxID=7227;
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Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lakako P., Lei Y., Lei Y., Lei Y., Lai Z., Liang Y., Lin X., Lai X., Lei Y., Lei Y., Lei Y., Lai Z., Liang Y., Lin X., Lai X., Lei Y., Lei Y., Lain X., Lai X., Martei B., McIntosh T.C., McLood M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mornt S.M., Moy M., Murphy B., Murphy D.M., Nelson D.L., Rabancton M., Nelson R.A., Nixon K., Nusskern D.R., Pacleb J.M., Rebon D.R., Sden K.A., Nixon K., Nusskern D.R., Pacleb J.M., Rehnert K., Sden Krämon S., Pollard J., Puri V., Reese M.G., Shenett K., Sden Krämos I., Simpson M., Skrupski M.P., Smith T., Spier E., Sperdling A.C., Stapleton M., Strong R., Sun E., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Rao Q.A., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., R. J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhao Q., Zhao X., Myels E.W., Rubin G.M., Venter J.C.;
R. The genome sequence of Drosophila melanogaster.";
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Rubin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G.,

A Agbayani A., Arcaina T.T., Baxter E., Blazej R.G., Butenhoff C.,

A Champe M., Chavez C., Chew M., Doyle C.M., Farfan D.E., Frise E.,

A Galle R., George R.A., Harris N.L., Hoskins R.A., Evans-Holm M.,

A Houston K.A., Hummasti S.R., Kim E., Li P., Moshrefi M., Pacleb J.M.,

RA Fark S., Sequeira A., Sethi H., Snir E., Svirskas R.R., Weinburg T.,

RA Full length Drosophila melanogaster cDNA sequence.";

RY Full length Drosophila melanogaster CDNA sequence.";

Brants AEO3736; AAFS5916.1; -.

DR EMBL; ARF45639; AAD38614.1; -.

DR FIBBase; FBG10027575; GBAB-B-R2.

DR InterPro: IPR000377; GPCR_Mgr.

InterPro: IPR000377; GPCR_Mgr.

RY Pfam; PF000037 Thm_3; L.

DR Pfam; PF000037 Thm_3; L.

DR Pfam; PF000037 Thm_3; L.

SEQUENCE 1221 AA; 138123 MW; A57A9954F31F0A05 CRC64;
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260 YSTDWMNVTQDSECSVEE-----IATALEG-----AILVDLLPLSTSGDIT
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4.0%; Score 254; DB 5; L
Best Local Similarity 17.9%; Pred. No. 1.4e-07;
Matches 213; Conservative 195; Mismatches 496;
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01-JUN-2002 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Metabotropic GABA B receptor subtype 2.
GABA-B-R2 OR BCDNA:GH07312 OR CG6706.
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterryota; Meoptera; Endopteryota; Diptera; Endopteryota; Ephydroidea; Drosophila;
LSSVAAFPXICTARAWILMAGFSLSFGAMFSKTWRVHSIFTDLKLNK-KVIKDYOLFMVV
                                                                                                             AYKGLLLVFGAFLAWETRHVSIPALNDSKHIGFSVYNVFITCLAGAAISLVLSDRKDLVF
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                                                                                          -----LLWGVYLCYAVRTVP-SAFHEPRYMAVAVHNELIISAIFHTIRFVLASRLQSDW
                                                                                                                                               MLMLYFAHTHLTVTVTVTIGLLLIPKFSHSSNNPRDDIATEAYEDELDMGRSGSYLNSSINS
                                                                                                                                                              AWSEHSLDPEDIRDELKKLYAQLEIYKRKKMITN-NPHLQKKRCSKKGLGRSIMRRITEI
                                                                                                                                                                                                                 PETVSRQ-----CSKEDKEGADHGTAKGTALIRKNPPESSGNTGKSKEETLKNRVFSLK
                                      AVILLVVFWFLIGW-TSSVCQNLEKQISLIGQGKTSDHLIFNMCLIDRWDYMTAVAEFLF
                                                               GVLLAIDIAIITTWQIADPFYRETKQLEPLHHENIDDVLVIPENEYCQSEHMTIFVSIIY
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Mezler M., Muller T., Raming K.;
"Cloning and functional expression of GABA-B receptors from
Drosophila.";
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Q9BML6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVILLVVFWFLIGW-TSSVCQNLEKQISLIGQGKTSDHLIFNMCLIDRWDYMTAVAEFLF 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----LLWGVYLCYAVRTVP-SAFHEPRYMAVAVHNELIISAIFHTIRFVLASRLQSDW 642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWRRKDGLGGDKSHF-----KWSPPYLEC-ENGSYKPGWLVTLSSAIYGLQPNLVPEFRG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            363 VLPVNNFRRRGPDQHISGSTKDVSEEAYVCLPCREGCPFCADDSPCFVQEDK----YLR 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVLLAIDIAIITTWQIADPFYRETKQLEPLHHENIDDVLVIPENEYCQSEHMTIFVSIIY 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MLMLYFAHTHLTVTVTVTIGLLLIPKFSHSSNNPRDDIATEAYEDELDMGRSGSYLNSSINS 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AWSEHSLDPEDIRDELKKLYAQLEIYKRKKMITNNPHLQKKRCSKKGLGRSIMRRITEIP 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ETVSRQCSKEDKEGADHGTAKGTALIRKNPPESSGNTGKSKEETLKNRVFSLKK----- 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OALIRKLGPEARKWIDGVTCTG------GSNVGSELEPILNDDIVRLSAPPVRRE 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              820 MPSTTVTEMTSVDSVTSTHVEMDNSFVSVQSTVMAPSLPPKKKKQSIVEHHSHAPAPTMM 879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLSGKKLTQKLKEDSEAESTESVPLVCKSASAHNLSSEKKTGHPRTSMLQKSLSVIASAK 910
                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       880 QPIQQQLQQHLQQHQQMQQQH----LQQQQHQQMQQQQQQQQHHHRHLEKRNSVSAQTD 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SASASVIGVITATVFLAFNIKY--RNQRYIKMSSPHLNNLIVGCMITYLSIIFLGLDTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSSVAAFPYICTARAWILMAGFSLSFGAMFSKTWRVHSIFTDLKLNK-KVIKDYQLFMVV
                                                                                                                                                                                                                                                                                                                                                              260 YSTDWWNVTQDSECSVEE-----IATALEG-----AILVDLLPLSTSGDIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 FLQATREESRILLQDLSSSAPHLANATLETEWFHGLRRK--WRPHLHRRGPNQGPRGLGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                303 VMKVDINLQKVDIDQCSSDGWFSGTHKCHLNNSECMPIKGLGFVLGAYECICKAGFYHPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAIISFQGLCMLLDFVSMLVVYHFRKAKSIRASGLILLETILFGSLLLYFPVVILYFEPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----TFRCILLRWARLLGFATVYGTVTLKLHRVLKVFLSRTAQRIPYMTGGRVMRML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VAGITADEYLVEYDRLRGT------EYSRFHGYTYDGIWAAALAIQYVAE-----
                                                                                                                                                                                                                                                                                    321;
                                                                                                                                                                                                                                        Length 1220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----DQTEESSSLPTESQEEETTEN---
                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                         1220 AA; 137976 MW; 2B33DA2C1A1BDA8B CRC64;
                                                                                                                                                                                                                                        5,
                                                                                                                                                                                                                                   Score 243.5; DB Pred. No. 6.4e-07 pred. No. 6.4e-07 pred. No. 6.4e-07 pred. Mismatches 48
                                                                  InterPro; IPR000337; GPCR_Mgr.
Pfam; PF00003; 7fm_3; 1.
Pfam; PF01004; ANF receptor; 2.
PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
                   FlyBase; FBgn0027575; GABA-B-R2.
InterPro; IPR001828; ANF_receptor
InterPro; IPR000337; GPCR_Mgr.
                                                                                                                                                                                                                                                                                    Conservative 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --SHSTYDHVR---
AF318273; AAK13421.1;
                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                Best Local Sim
Matches 212;
                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                     Receptor
                                                                                                                                                                                                                                                                                                                                   72
                                                                                                                                                                                                                                                                                                                                                                                                                              131
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RAMIN-BERKELEK;

RAMIN-BERKELEK;

RADIANN-BERKELEK;

RADIANN-BERKELEK;

RADIANN-BERKELEK;

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RADIANN-BERGER;

RADIANN-BERGER;

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RADIAND-BERGER;

                                                                                                                                                                                                                                                                                                                   992 STSQSELSNMCPHSKPSTP---AVIK----TPTASDHRRTSMGSALKSNFVVSQSDLMDT 1044
                                                                                 ETKDPAPQNSNPAEEPRKPQKSGIMKQQRVNPTTANSDLNPGTTQMKDNFDIGEVCPWEV 1011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                   1012 YDL------FSLKEKSHHKPKAAEVC
                                                                                                                                                                           : | : | | : | | : | | : | | 1045 HILSHAKQRQSPRNYASPQRCAEHHGGHGMTYDPNTJSPIQRSVSEKNRNKHRPKP----
                                                                                                                                                                                                                                                             -----QKGTVC--QSETDSERERDPPNSQPCVQPRKVS-----RSSNIQHAAHH
              ---SQKPLPKDKETNRNHSNSDNT
                                                                                                                                                                                                                         1059 QQSNQKRIDKAEVCLWESQGQSILEDEKLLISKTPVLPERAKEENGGQPRAANVCAGQSE
                                                                                                                                                                                                                                                                                              1119 ELPPKAVASKTENENLNQIGHQEKK---TSSSEENVRGSYNSSNNFQQPLTSRA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
              EKTLGLAGKTQTAG------VEERTK--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                    1170 ----EVCP 1173
                                                                                                                                                                                                                                                                                                                                                                                                     1201 SAVGOSCP 1208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CG18679 protein.
CG18679.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9W1P4
Q9W1P4;
                                              935
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                                                                                                                                                                                                                                                             1101
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Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang S., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wall Jams C.M., Weinstock G.M., Weissenbach J., Yelliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
EMBL: AB003040663; CG18679.
SEQUENCE 176 AA, 19661 MW; 524E4E2C48CB7D33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 RGVMKVDINLQKVDIDQCSSD-----GWFSGTHKCHLNNSECMPIKGLGFVLGAYE 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     352 CICKAGFYHPGVLPVNNFRRRGPDQHISGSTKDV-----SEEAYVCLPCRE 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273 -ENGSY------KPGWLV-TLSSAIYGL---QPNLVPEFRGVMKVDIN 309
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Storjohann L.L., Stormann T.M., Parks T.N.;
"Molecular Cloning and Functional Expression of Chick Metabotropic Glutamate Receptor 5 Splice Variants.";
Submitted (JAN-2000) to HEMBL/GenBank/DDBJ databases.
EMBL; AF227203; AAK01488.1; -.
InterPro: IPR001828; ANF_receptor.
InterPro: IPR001828; ANF_receptor.
Pfam; PF001094; ANF_receptor.
Pfam; PF01094; ANF_receptor, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.7%; Score 237.5; DB 13; Length 1242; 9.3%; Pred. No. 1.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         219 ETEWFHGLRRKWRPHLHRRGPNQGPRGLGHSWRRKDGLGGDKSHFKWSPPYLEC---
                                                                                                                                                                                                                                                                                                                                                                             5; Length 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1242 AA; 138063 MW; 9ED84AFEFA2CF0EB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  398 GCPFCADDSPCFVQEDKYLRLAIISFQGLCMLLDFVSMLVVYHFR 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Metabotropic glutamate receptor 5 splice variant f.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCDSCEDSSPCIAALNWPMRTSILAL - - ACIVIGLLPPAAWFTFR
                                                                                                                                                                                                                                                                                                                                                                    Score 238.5; DB 5
Pred. No. 8.5e-08;
5; Mismatches 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1242 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1. PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1. PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1. PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
                                                                                                                                                                                                                                                                                                                                                                             31.5%; Pt. 25; }
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 209; Conservative 142;
                                                                                                                                                                                                                                                                                                                                                                       3.78;
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                                                                                                                                                                                                                                                                                                                                                                                               Local Similaricy
hes 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Receptor.
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                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouerv Match
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Matches
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SGIMKQ--QRVNPTTAN-SDLN-----PGT---TQMKDNFDIGEVCPWEVYDLTPGP 1018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGLAGKTQTAGVEERTKSQKPLPKDKETNRNHSNSDNTETKDPAPQ-NSNPAEEPRKPQK 972
                 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                             574 LIDRWDYMTAVA-EFLFLLWGVYLCYAVRTVPSAFHEPRYMAVAVHNELIISAIFHTIRF 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGK-------KTGNCVSLIVPQQDCQLQDLLKHSNGKSVSWAQNEKSSRGAHLW 990
                                                                                                                                                                                                                                                      ---LAIISFQGLCMLLDFVSMLVVYHFRKAKSIRASGLILLETILFGSLLLYFPVVILYF 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLASRLQSDWMLMLYFAHTHLTVTVTIGLLLIPK----FSHSSNNPRDDIATE-AYEDEL 687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GSNYKIITMCFSVSLSATVALGCMFVPKVYIILAKPERNVRSAFTTSTVVRMHV 853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                854 GDGKSSSAASRSSSLVNLWKRRGSSGETLR------YKGRRLA---PHKSEIEC 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   746 -SKKGL----GRSIM--RRITEIPETVSRQCSKEDKEGADHGTAKGTALIRKNPPESSGN 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGKSKEETLKNRVFSLKKSHSTYDHVRDQTEESSSLPTESQEEETTENSTLESLSGKKLT 858
                                                                                 ------MKPIDGRKLL----ESLMKTNFTGVSGDMILFD
                                                                                                                                                                                                      GQIKVIRKGEVSCCWTCTPCKENEYVPDEYTCKACQLGSWPNDELJGCDLIPVQYLRWGD
                                                                                                                                                                                                                                                                           ------LVIAFILI-----CIQLGIIVALFIMEPPDIMHDYPSIREVYLIC
                                                                                                                                                                                                                                                                                                                                                                                           MTGGRVMRMLAVILLVVFWFLIGWTSSVCQNLEKQISL-----IGQGKTSDHLIFNMC
                                                                                                                                                 ENGDSPGRYEIMNFKKMGKDYFDYINVGSWDNGELKMDDDEIWSEKNNIIRSVCSEPCEK
                                                                                                                                                                                    ------AYVCLPCREG------CPFCA-----DDSPCFVQEDKYLR---
                                                                                                                                                                                                                                                                                                                          EPSTFRCILLRWARLLGFATVYGTVTLKLHRVLKV--------FLSRTAQRIPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DMGRSGSYL - - NSSINSAWSEHSLDPEDIRDELKKLYAQLEIYKRKKMITNNPHLQKKRC
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----HPGVLPVNNFRRRGPD--QHI-----SGSTKDVSEE------
                                                 LQKVDIDQCSSDGWFSGTHKCHLNNSECMPIKGLGFVLGAYECICKAGFY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1144 MTTFAEIOPLPSIEVNGASOSARKOSNGSVKEGTAETPSAK------
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**QSSS 1240** 

1237

RESULT 11

59; Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endropeda; Tracheata; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. 63 RSTDGTILAQKLAEEVPMDVASYLYTGDSHQLKRANCSGR-----YELAGLPGKWP--A 114 115 LASAHPSLHRALDTL----TH-----ATNFLNVMLQSNKSREQNLQDDLDWYQALVW 162 ----ILLQDLSS 208 --FHGQDGFG-----SGYGPRISIAATQSDSRRRRRGVVGTSGGHLFPEAISQ 490 SAPHLANATLETEWFHGLRRKWRPHLHRRGPNQGPRGLGHSWRRKDGLGGDKSHFKWSPP 268 491 YAPQ----TYDAVWAIALALRAAEEHWRRNEEQS------KLDGFDYTRSDMAWE-- 535 ---CENGSYKPGWLVTLSSAIYGLQPNLVPEFRGVMKVDINLQKVD 314 IDQCSSDGWFSGTHKCHLNNSECMPIKGLGFVLGAYECICKAGFYHPGVLPVNN--FRRR 372 -----AFYTIATLSSVGIALAITF 639 433 VSMLVVYHFRKAKSIRASGLILLETILFGSLLLYFPVVILYFEPST-----FRCILLR 485 WARLL--GFATVYGTVTLKLHRVLKVFLSRTAQ------RIPYMTGGRVMRMLAVI 533 344 RETDTRIIIGSFSQELAPQILCEAY-----RLRMFGADYAWILHESMGAPW-WPDQR 373 GPDQHISGSTKDVSEEAYVCLPCREGCPFCADDSPCFVQEDKYLRLAIISFQGLCMLLDF Indels 416; GABA-B receptors from 1305 AA; 143701 MW; 8BBFA80F0E9BEADD CRC64; 01-JUN-2001 (TrEMBLrel. 17, Created) 01-JUN-2001 (TrEMBLrel. 17, Last sequence update) 01-JUN-2002 (TrEMBLrel. 21, Last annotation update) Conservative 183; Mismatches 396; Putative metabotropic GABA-B receptor subtype 3. GABA-B-R3 OR CG3022. Score 232; DB 5; Pred. No. 3.9e-06; PROSITE; PSS0259; G\_PROTEIN\_RECEP\_F3\_4; 1.
PROSITE; PS00041; HTH\_ARAC\_FAMILY\_1; UNKNOWN\_1. SLLEGEPSISRAAITFSTDSLSAPAPQVFLQATREESR--PRT; 1305 AA SEQUENCE FROM N.A. MEDILIPS=21097320; PubMed=11168554; Mediler T., Raming K.; "Cloning and functional expression of EMBL, AF318274; AAK13422.1; -... Flybase; FB90031275; GABA-B-R3. InterPro; IPR001828; ANF\_receptor. InterPro; IPR0000337; GPCR\_MGr. InterPro; IPR000005; HTHARAC. Pfam; PF001094; ANF\_receptor; IPfam; PF01094; ANF\_receptor; IPfam; PF01094; ANF\_RECEPTOR; IPRINTS; PR00248; GPCRMGR. Drosophila melanogaster (Fruit fly) J. Neurosci. 13:477-486(2001) 3.6%; Similarity 18.6%; PRELIMINARY; YLE-----Best Local Simi Matches 228; Drosophila. SEQUENCE Receptor Query Match 536 395 163 444 569 315 578 614 486 869 DDT TDD TD g δý Db òγ g Dp pp g δy 음 g g à δλ Qγ à ŏ Qγ

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943 DAEIRKLERLLESGLTTTSTTTSSTSL--LTGGGHLKPELTVTSGISOTPAASKNRTPS 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1183 GDQTLG-----GKYVKLLETKVNFQLPSNRRPSVVQQPPSLRERVRGSPRFPHRILP 1234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             954 KDPAPQNSNPAEEPRKPQKSGIMKQQRVNPTTANSDLNPGTTQMKD-NF-DIGEVCPWEV 1011
                                                                                                                                                                                                                                                                                        891 IWARNDIIDPVIHSMGLKMECNTRRFVVDDRRELQYRVEVQNRVYKKE------IQAL 942
                                                                                                                                                                                                                                                                                                                                                                                                                  795 SSGNTGKSKEETLKNRVFSL-----KKSHSTYDHVRDQTEESSSLPTESQEEETTENST 848
                                                                                                      809.GLLLVVGVYMAWETRHVKIPALNDSQYIGVSVYSVVITSAI-----VVVLANLISERVTL 863
                                                                                                                                                                 LYFAHTHL---TVTVTIGLLLIPKFSHSSNNPRDDIATEAYEDELDMGRSGSYLNSSINS 702
                                                                                                                                                                                                                                                  703 AWSEHS-LDP-------EDIRDELKKLYAQLEIYKRKKMITNNPHLQKK 743
                                                                                                                                                                                                                                                                                                                                 744 RCSKKGLGRSIMRRITEIPETVSRQCSKEDKEGADH------GTAKGTALIRKNPPE 794
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NCBI_TaxID=7227;
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LLVVFWFLIGWTSSVCQNLEKQISLIGQGKTSDHLIF----NMCL---IDRWDYMTAVAE 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRISMLOKSLSVIASAKEKTLGLAGKTQTAGVEERTKSOKPLPKDKETNRNHSNSDNTET
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                                                                              FLFLLWGVYLCYAVRTVP-SAFHEPRYMAVAVHNELIISAIFHTIRFVLASRLQSDWMLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     849 LESLSGKKLTQKLKEDSEAESTESVPLVCKSAS-----AHNLSSEKKTG-----H
                                     LLVTLWVVTDPMERHLHNLTLEIS-----ATDRSVVYQPQVEVCRSQHTQTWLSVLYAYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1001 ISG-----ILPNLLLSVLPPVIPRASWPSAEYMQIPMRRSVTFASQPQLEE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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Drosophila melanogaster (Fruit fly).
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RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ra Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Berman B.P., Bandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brockstein P., Bottler P., Ra Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Caarley S., Dahlke C., Davenport L.B., Davies P., Chandra I., Ra de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., Bodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Ra Durbin K.J., Evangelista C.C., Ferraz C., Ferriar S., Ferischmann W., Ra Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Ra Dorbin K.J., Evangelista C.C., Ferraz C., Ferriar S., Ferischmann W., Rarrish D., Houston K.A., Howland T.J., Hernandez J.R., Houck J., Rarrish D., Houston K.A., Howland T.J., Hernandez J.R., Hockhum K.A., Andrein B.L., Kalnsh F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jalain M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Jalain M., Mattei B.L., Modia C.D., Kraft C., Kravitz S., Kulp D., Liai Z., Rasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Martei B.L., Motina C.D., Kraft C., Kravitz S., Kulp D.M., Nelson D.R., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.R., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Rannett K., Semidton K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Stugski M.P., Smith T., Raying S., Yeb N., Wodage T., Worlex E., Wang S., Pan S., Pallams S.M., Wodage T., Worlex E., Wang S., Pan S., Pallams S.M., Wodage T., Worlex E., Wang S., Pan S., Pallams S.M., Wodage T., Worlex E., Wang S., Pan G., Zhen                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DSLSAP-APQVFLQATREESRILLQDLSSSAPH-----LANATLETEWFHGLRRKWRP 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------RAAEEHW-----RRNEEQ 519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----ADDSPCFVQEDKYLRLAIISF 423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1305;
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PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
SEQUENCE 1305 AA; 143588 MW; A9C3C85307650450 CRC64;
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18.8%; Pred. No. 7.5e-06;
ive 171; Mismatches 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE003588; AAF51465.2;
FlyBase; FBgn0031275; GABA-B-R3.
Interpro; IPR0001828; ARE_receptor.
Interpro; IPR000337; GPCR_MGr.
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Pfam; PF01094; ANF_receptor; 1.
PRINTS; PR00248; GPCRMGR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            389 AYVCLPCREG----CPFC----
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Eukaryota: Metazoa: Arthropoda; Tracheata; Hexapoda; Insecta;
Plerygota; Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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StapLeton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
| : : | | | : : | : | : | : | | : | DSFATVCTARVYLLSAGFSLAFGSMFAKTYRVHRIF-TRTGSVFKDKMLQDIQLILLVGG
                                                                                                       RVMRMLAVILLVVFWFLIGWTSSVCQNLEKQISLIGQGKTSDHLIF ---- NMCL---IDR
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01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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                                                                                                                                                                             633 VLASRLQSDWMLMLYFAHTHLTVTVTIG-----LL-----LIPKFSHSSNNP----- 674
                                                                                                                                                                                                    235 IISSSTEGSW-----ESHISTDSSIGSKVESLLIEALYSLIQESSSSSESPVSNEPST 287
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterryota; Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                       288 GATDDSSSTESLPDSTQESSSSESPVSFELSTEATNESSSSESLPNSSTQDSSSSTETS 347
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G.M.,
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Papagiannakis G., Spanos L., Siden-Klamos I., Louis C.;
"Sequencing the distal X chromosome of Drosophila melanogaster.";
                                                                                                   ; Score 225; DB 5; Length 1514;
; Pred. No. 1.3e-05;
91; Mismatches 281; Indels 128;
                                                 EMBL; AYO73323; AAL68190.1; -. SEQUENCE 1514 AA; 157140 MW; 1FFC4B0664105AD5 CRC64;
                               (JAN-2002) to the EMBL/GenBank/DDBJ databases
Phouanenavong S., Wan K., Yu C., Lewis S.E.,
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Brain Res. Mol. Brain Res. 73:93-103(1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1103 NGGQPRAANVCA--GQSEELP-----PKAVASKTENENLNQIGHQEKKTSSSEENVR 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : : i :| | : :: | | :: | SRRESVADSSVEDESKGASRPESVVDSVKDEAEKQESRRESKTESVIPPKA 2214
                                                                                                                                                                                                                                                                                E----SRRESVAEKSPLPSKEAS------RPASVAESIKDEAEKSKEESRRESVAE 1821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2111 RRESMAESGKAQSIKGDQSPLKEVSRP----ESVAESVKDD------PVKSKEP 2154
                                                                                                                                                                                              668 SHSSNNPRDDIATEAYEDELDMGRSGSYLNSSINSAWSEHSLDP----EDIRDELKKLYA 723
                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1153 GSYNSSNNFQQPLTSRAEVCPWEFETPAQPNAGRSVALPASSALSANKIAGPRKEE 1208
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                  GTALIRK--NPPES-----SGNTGKSKEETLKNRVF-----SLKKSHSTYDHVRDQT
                                                                                                                                                                                                                                                                                                                                        KSAS----AHNLSSE---KKTGHPRTSMLQKS-----LSVIASAKEKTLGLAGKTQTA
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                                                                                                                                  Query Match 3.5%; Score 225; DB 5; Length 5327; Best Local Similarity 21.5%; Pred. No. 8.1e-05; Matches 128; Conservative 91; Mismatches 277; Indels 100;
                                                                                                      FEFEE23A118FF38A CRC64;
 to the EMBL/GenBank/DDBJ databases
                                                       Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases
EMBL; AL031128; CAA200066.1; -
FlyBase; FBGN0015390; futsch.
SEQUENCE 5327 AA; 575942 MW; FEFEE23A118FF38A CRC64
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STRAIN=ICR; TISSUE-BRAIN;
MEDLINE=2005087: pubMed=10581402;
Zhu H., Ryan K., Chen S.;
"Cloning of novel splice variants of mouse mGluRl.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2001 (TrEMBLrel. 16, Created)
01-077-2001 (TrEMBLrel. 18, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Metabotropic glutamate receptor type 1.
GPRCIA OR GJUSH.
Mus musculus (Mouse).
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(TrEMBLrel. 18, 1
(TrEMBLrel. 19,
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Submitted (JUL-1998)
                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 222.5; DB 11; Length 1199;
Pred. No. 1.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                           1199 AA; 133211 MW; FE5370AF160CC16E CRC64;
                                              Zhu H., Ryan K., Chen S.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL: AF320126; AAG41991.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----TAVIK---PLTKSYQGSGKSLTFSD---
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                                                                                                                                                                                                                                  Pfam; PF01094; ANF_receptor; 1.
PRINTS; PR00248; GPCRMGR.
PROSITE; PS00979; G_PROTEIN_RECEP_F3_1;
PROSITE; PS00980; G_PROTEIN_RECEP_F3_2;
PROSITE; PS00981; G_PROTEIN_RECEP_F3_2;
PROSITE; PS50259; G_PROTEIN_RECEP_F3_3;
                                                                                                                            MGD; MGI:1351338; Gprcla.
InterPro; IPR001B28; ANR_receptor.
InterPro; IPR000337; GPCR_Mgr.
Pfono; 7fm_3; 1.
SEQUENCE FROM N.A.
STRAIN=ICR; TISSUE=BRAIN;
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Search completed: February 15, 2003, 08:30:53 Job time: 86.6488 secs

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Steuart Street Tower, One Market Plaza
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CLASSIFICATION: 435
PRIOR APPLICATION 1435
PRIOR APPLICATION NUMBER: US/07/648,481
FILING DATE:
APPLICATION NUMBER: US 07/626,806
FILING DATE: 12-DE-1990
ATTOCNEY AGGNT INFORMATION:
NAME: PAITHER, Steven W
REGISTRATION NUMBER: 31,990
                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 94105
ZIP: 94105
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/041,538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 206-623-6793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
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; MOLECULE TYPE: protein
US-08-041-538-2
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                  USA
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1524.948 Million cell updates/sec
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                                                                                                            US-09-775-181-2
6382
1 MGAMAYPLLICLLLAQLGLG......LSANKIAGPRKEEIWDSFKV 1215
                                                                     February 13, 2003, 00:11:08; Search time 23.4427 Seconds
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
          GenCore version 5.1;3 Copyright (c) 1993 - 2003 Compugen Ltd
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US-08-367-264-10
US-08-072-574-8
US-08-538-526-1
US-08-687-289A-8
US-08-687-289A-8
US-08-687-289A-9
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US-08-486-270-8
US-08-367-264-8
US-09-153-757-8
US-08-660-148-5
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US-08-687-289A-6
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US-08-465-157-2
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Maximum Match 100%
Listing first 45 summaries
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Length 1199;

Score 220.5; DB 1; Pred. No. 3e-09;

3.5%; 18.6%;

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                                                                                                                                                                                                                     Sequence 49,
Sequence 12,
                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Mulvhill, Eileen R
APPLICANT: Hagen, Frederick S
APPLICANT: Housened, Khaled M
APPLICANT: Housened, Khaled M
APPLICANT: Almers, Wolfhard
TITLE OF INVENTION: G PROTEIN COUPLED GLUTAMATE
TITLE OF INVENTION: RECEPTORS
TUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
           US-08-480-751-8

US-08-943-986-8

US-08-943-986-8

US-08-484-7198-8

US-08-484-159-8

US-08-486-270-12

US-08-367-264-12

US-08-296-791-6

PCT-US95-10661A-6

US-08-96-791-6

US-08-96-791-6

US-08-96-791-6

US-08-96-791-6

US-08-96-791-6

US-08-986-106-2

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FITLE OF INVENTION:
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                                                                                                                                             ZIP: 94105
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                                                                                          CITY: Sa
STATE: C
COUNTRY:
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                                      ----AYVCLPCREG- 398
                                                                                                             -----CPFC-----ADDSPCFVQEDKYLR-----LAIISFQGLCMLLDFVSMLVV 438
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                                                                   GTWHEGVLNIDDYKIQ --- MNKSGMVRSVCSEPCLKGQIKVIRKGEVSCCWICTACKENE 554
                                                                                                                                             555 FVQDEFTCRACDLGWWPNAELTGCEPIPVRYLEWSDIESIIAIAFSCLGILVTLFVTLIF 614
                                                                                                                                                                                    439 YHFRKAKSIRASGLILLETILFGSLLLYFPVVILYFEPSTFRCILLRWARLLGFATVYGT 498
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Conservative 120; Mismatches 330; Indels 265;
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APPLICANT: Mulvihill, Eileen R
APPLICANT: Hagen, Frederick S
APPLICANT: Hommed, Khaled M
APPLICANT: Hommed, Wolfhard
TITLE OF INVENTION: G PROTEIN COUPLED GLUTAMATE
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                                    GFYHPGVLPVNNFRRGPDQHISGSTKDVSEE----
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Matches 163;
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US-08-463-642-2
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                                                                             Tower, One Market Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 163; Conservative 120; Mismatches 330;
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Pred. No. 3e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA.

APPLICATION NUMBER: US 07/672,007
FILING DATE: 18-MAR-1991
APPLICATION NUMBER: US 07/648,481
FILING DATE: 30-JAN-1991
APPLICATION NUMBER: 07/626,806
FILING DATE: 12-DEC-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,642
FILING DATE: 05-UUN-1995
                                                  ADDRESSEE: Townsend and Townsend STREET: Steuart Street Tower, On
                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 3.5%;
Best Local Similarity 18.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 206-623-6793
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Parmelee, Steven W REGISTRATION NUMBER: 31,9
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NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                                                     San Francisco
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----IFRRKKPGAGNANSNGKSVSWSEPGGRQAPKGQHVWQRLSVHVKT 919
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                                                                                                                     765 VSRQCSKEDKEGADHGTAKGTALIRKNPPESSGNTGKSKEETLKNRVFSLKKSHSTYDHV 824
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STREET: Steuart Street Tower, One Market Plaza
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APPLICANT: Mulvihill, Eileen R
APPLICANT: Hagen, Frederick S
APPLICANT: Housmed, Khaled M
APPLICANT: Almers, Wolfhard
TITLE OF INVENTION: G PROTEIN COUPLED GLUTAMATE
TITLE OF INVENTION: RECEPTORS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1112 VCAGQSEELPP--KAVASKTENENLNQIGHQEKKTSSS 1147
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REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-6-1-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,602
FILING DATE: 31-MAY-1995
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FILING DATE: 18-MAR-1991
APPLICATION NUMBER: US 07/648,481
ELLING DATE: 30-JAN-1991
APPLICATION NUMBER: 07/66,806
FILING DATE: 12-DEC-1990
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ATTORNEY/AGENT INFORMATION:
NAME: Darman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08455602
Patent No. 5747267
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PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy
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STATE: CA
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                                                                                                                                                           3.5%; Score 220.5; DB 1;
ilarity 18.6%; Pred. No. 3e-09;
Conservative 120; Mismatches 330;
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                                                                                                                                                             Query Match 3.5%;
Best Local Similarity 18.6%;
                  2
                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1199 amino acids
 206-623-6793
                  INFORMATION FOR SEQ ID NO:
                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-455-602-2
                                                                      TYPE: amino acid
TELEFAX:
                                                                                                                                                                                                163;
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                                                                     -----IFRRKKPGAGNANSNGKSVSWSEPGGRQAPKGQHVWQRLSVHVKT 919
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                                           PSAFHEPRYMAVAVHNELIISAIFHTIRFVLASRLQSDWMLMLYFAHTHLTVTVTIGLLL 663
                                                                                                                                IPK----FSHSSNNPRDDIATEAYEDELDMG------RSGSYLNSSINSAWSEHSLDP 711
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-----MEPPMPILSYPSIKE--VYLICNTSNLGVVAPVGYNGLLIMSCTYYAFKTRNV 777
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APPLICANT: Hagen, Frederick S.
APPLICANT: Hagen, Frederick S.
APPLICANT: Housmed, Khaled M.
APPLICANT: Housmed, Khaled M.
APPLICANT: Almers, Wolfhard
TITLE OF INVENTION: G PROTEIN-COUPLED GLUTAMATE RECEPTORS
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOwnsend and Townsend
                                                                                                                                                            ----TAVIK---PLTKSYQGSGKSLTFSD----
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CITY: San Francisco
STATE: California
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/09422
FTITING DATE: 19911212
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/672,007
FILING DATE: 18-WAR-1991
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application PC/TUS9109422 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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OPERATING SYSTEM:
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                                                                                                                                     APPLICANT: Hagen, Frederick S
APPLICANT: Hagen, Frederick S
APPLICANT: Hoummed, Khaled M
APPLICANT: Almers, Wolfhard
TITLE OF INVENTION: G PROTEIN COUPLED GLUTAWATE
TITLE OF INVENTION: RECEPTORS
TUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Parmelee, Steven W
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-6-1
TELECOMMUNICATION INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/041,538
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,157
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                                                              Sequence 2, Application US/08465157
Patent No. 5869609
                                                                                                                              APPLICANT: Mulvihill, Eileen R
APPLICANT: Hagen, Frederick S
APPLICANT: Houamed, Khaled M
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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INFORMATION FOR SEQ ID NO: 2:
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LENGTH: 1199 amino acids
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206-623-6793
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                                                                                                         GENERAL INFORMATION:
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                    RESULT 4
US-08-465-157-2
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                Krapcho, Karen J.
Hammerland, Lance G.
VENTION: CHIMERIC RECEPTORS AND METHODS FOR VENTION: TENEVELY COMPOUNDS ACTIVE AT VENTION: THE USE OF SUCH COMPOUNDS IN THE VENTION: THE USE OF SUCH COMPOUNDS IN THE VENTION: TREATMENT OF NEUROLOGICAL DISORDERS VENTION: AND DISEASES
                                                                                                                                                              1112 VCAGQSEELPP--KAVASKTENENLNQIGHQEKKTSSS 1147
                                                                                                                                                                                                   1160 VASGSSVPSSPVSESVLCTPPNVTYASVILRDYKOSSS 1197
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OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FASTSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,289A
FILING DATE: July 25, 1996
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/001,526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 220/004
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Lyon & Lyon STREET: 633 West Fifth Street STREET: 814 4700 CITY: Los Angeles STATE: Callfornia COUNTRY: U.S.A. 21P: 90071-2066
                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/08687289A Patent No. 5981195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: July 26, 1995
ATTORNEY/AGENT INFORMATION:
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 6
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Matches 174; Conserv
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                                                                                                                                                                                                                                                                          RESULT 6
US-08-687-289A-6
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSAFHEPRYMAVAVHNELIISAIFHTIRFVLASRLQSDWMLMLYFAHTHLTVTVTIGLLL 663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                3.5%; Score 220.5; DB 5; 18.6%; Pred. No. 3e-09;
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                                                                                                                                                                                   13952-6PC
APPLICATION NUMBER: US 07/648,481 FILING DATE: 30-JAN-1991 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/626,806 FILING DATE: 12-DEC-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                              NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1199 amino acids
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CORRESPONDENCE ADDRESS:
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Patent No. 621353
GENERAL INFORMATION:
APPLICANT: Burnett, J. P.
APPLICANT: Mayne, Nancy G.
APPLICANT: Sharp, Robert L.
APPLICANT: Sharp, Robert L.
TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND TITLE OF INVENTION: RELATED NUCLEIC ACID COMPOUNDS NUMBER OF SEQUENCES: 6
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 LPVNNFRRRGPDQH----ISGSTKDVSEE----AYVCLPCREG---
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                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,148
ADDRESSEE: Ell Lilly and Company
STREET: Lilly Corporate Center
STATE: Indianapolis
STATE: Indiana
COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/282,853
                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTATION UNMER: 36,808
REFERENCE/DOCKET NUMBER: X-941
RELECOMMUNICATION INFORMATION:
TELEFONE: (317) 276-0756
TELEFAX: (317) 276-0756
TELEFAX: (317) 276-0756
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                            ZIP: 46285
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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APPLICANT: Ellis, Steven B.
APPLICANT: Liaw, Chen
APPLICANT: Liaw, Chen
APPLICANT: Johnson, Edwin C.
APPLICANT: Hess, Stephen D.
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF
                               823 YIILAKPERNVRSAFTTSTVVRMHVGDGKSSSAASRSSSLVNLWKRRGSSGETLSSNGKS
                                                                      -----LYAQLEIYKRKKMITNNPHLQK---KRCSKKGLGRSIMRRITEIPE
                                                                                                                                                                                                     824 VRDQTEESSSLPPTESQEEETTENSTLESLSGKKLTQKLKEDSEAESTESVPLVCKSASAH
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---FSHSSNNPRDDIATE-AYEDELDMGRSGSYL--NSSINSAWSEHSLDPEDIRDELKK
                                                                                                                                     764 TVSRQCSKEDKEGADHGTAKGTALIRKNPPESSGNTGKSKEETLKNRVFSLKKSHSTYDH
                                                                                                                                                                     -----AGAG-GSAGGVGATGGAGCAGAGPGGPESPDAGPKALY------
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                                                                                                  VTWAQNEKSSRGQHLWQRLSIHINKKENPNQTAVIKPFPKSTESRGLGAG--
                                                                                                                                                                                                                                                                          NLSSEKKTGHPR-TSMLQKSLSVIASAKEKTLGLAG------
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444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/486,270
FILING DATE: U2-JUN-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                            ANSDLNPGTTQMKDNFDIGEVCPWEVYDLTPGPVPSESK 1024
                                                                                                                                                                                                                                                                                                                                                                                                                                              -----FRDSVDSGSTTPNSPVSESALCIPSSPK 1164
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APPLICATION NUMBER: US 08/072,574
FILING DATE: 04-JUN-1993
ATTORNEY AGENT INFORMATION:
NAME: Reiter, Stephen E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/08486270 Patent No. 5807689 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: FP41
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
TELEFAX: 619-546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Pretty,
STREET: 444 South F
CITY: Los Angeles
STATE: CA
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                                                                                                                                                                                                                                                                                                                    -------KPGWLV-TLSSAIYGL---QPNLVPEFRGV-------MKVD
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                                                                                                                                                               Matches 178; Conservative 116; Mismatches 401; Indels 248;
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                                                                                                                      Length 1180;
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                                                                                                                   Score 200; DB 1;
Pred. No. 1.6e-07;
                                                                                                                      3.1%;
18.9%;
                 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-486-270-8
amino acid
                                                                                                                                          Similarity
                                                                                                                      Query Match
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ADDRESSES: Pretty, Schroeder, Bru
STREET: 444 South Flower Street,
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
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Ellis, Steven B.
Liaw, Chen
Pontsler, Aaron
Johnson, Edwin C.
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Patent No. 6413764
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COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
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US-09-153-757-8
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                                                                                                        APPLICANT: Daggett, Lorrie
APPLICANT: Ellis, Steven B.
APPLICANT: Liaw, Steven B.
APPLICANT: Liaw, Chan
APPLICANT: Johnson, Edwin C.
APPLICANT: Hess, Stephen D.
TITLE OF INVENTION: HUGLEIC ACIDS ENCODING SAME AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----AYVCLPCREG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 18.9%; Pred. No. 1.6e-07;
Matches 178; Conservative 116; Mismatches 401; Indels 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1180;
                                                                                                                                                                                                                                                                                           ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US.08/072,574
FILING DATE: 04-UN-1993
ATTORNEY/AGENT INFORMATION:
NAME: REILER, SLEPHEN E.
REFERENCE/DOCKET NUMBER: 31,192
REFERENCE/DOCKET NUMBER: 91,192
TELEPHONE: 619-546-4737
TELEPHONE: 619-546-4737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FP41 9772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/367,264
FILING DATE: 02-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                   Sequence 8, Application US/08367264
Patent No. 6001581
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CORRESPONDENCE ADDRESS:
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                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     USA
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                                    US-08-367-264-8
                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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1080 FAE----IQPLPAIEVTGGAQPAAGAQAAGDAARESPAAGPEAAAAKPDLEELVALTPP 1134
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                                                                                                                           LEKQISL-----IGQGKTSDHLIFNMCLIDRWDYMTAVA-EFLFLLWGVYLCYAVRTV 603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      717 ELKK------LYAQLEIYKRKKMITNNPHLQK---KRCSKKGLGRSIMRRIT 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          760 EIPETVSRQCSKEDKEGADHGTAKGTALIRKNPPESSGNTGKSKEETLKNRVFSLKKSHS 819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  820 TYDHVRDQTEESSSLPTESQEEETTENSTLESLSGKKLTQKLKEDSEAESTESVPLVCKS 879
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                                                                                                                                                                                                                                                                                                                                                                                               PSAFHEPRYMAVAVHNELIISAIFHTIRFVLASRLQSDWMLMLYFAHTHLTVTVTIGLLL 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   765 PANFPEAKYIAFTMYTTCIIWLAFVPIYF-----GSNYKIITMCFSVSLSATVALGCMF 818
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                                                                               --FLSRTAQRIPYMTGGRVMRMLAVILLVVFWFLIGWTSSVCQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           819 VPKVYIILAKPERNVRSAFTTSTVVRMHVGDGKSSSAASRSSSLVNLWKRRGSSGETLSS
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lower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/153,757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             982 NPTTANSDLNPGTTQMKDNFDIGEVCPWEVYDLTPGPVPSESK 1024
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--AGAG-GSAGGVGATGGAGCAGAGPGGPESPDAGPKALY----- 969
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-Doc // SOFTWARE: Pa+r---
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US-08-660-148-5
; Sequence 5, Application US/08660148
; Patent No. 6211353
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REGISTRATION NUMBER: 36,808
REPERENCE/DOCKET NUMBER: X - STELECOMMUNICATION INFORMATION:
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TELEFAX: (317) 276-3861
INFORMATION FOR SEQ ID NO: 5:
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CORRESPONDENCE ADDRESS:
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nes 207; Conserv
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APPLICANT: Burnet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Indiana
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US-08-660-148-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        219 ETEWFHGLRRKWRPHLHRRGPNQGPRGLGHSWRRKDGLGGDKSHFKWSPPYLECENGSY- 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            308 INLOKVDIDQCSSDGWFSGTHKCHLNNSECMPIKGLGFVLGAYECICKAGFYHPGVLPVN 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----FLSRTAQRIPYMTGGRVMRMLAVILLVVFWFLIGWTSSVCQN 551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 3.1%; Score 200; DB 4; Length 1180; Best Local Similarity 18.9%; Pred. No. 1.6e-07; Matches 178; Conservative 116; Mismatches 401; Indels 248;
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                                                      ATTOMACTOR NUMBER: US/08/486,270
FILING DATE: 02-JUN-1994
APPLICATION NUMBER: US 08/072,574
ATTOMACTOR OF 04-JUN-1993
ATTOME/AGENT INFORMATION:
NAME: Relter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: FP41 9772
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
TELEFAX: 619-546-4392
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1180 emino acids
                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                     <Unknown>
FILING DATE: 15-Sep-1998
CLASSIFICATION: <Unknown:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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                                                                 ----DVAEAEEHFPAPARPRSPSPISTLSHRAG----SASRTDDDVPSLHSEPVARSS 1019
                                                                                                                                                                                                                                                                                                                                                  1080 FAE----IQPLPAIEVTGGAQPAAGAQAAGDAARESPAAGPEAAAAKPDLEELVALTPP 1134
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TYDHVRDQTEESSSLPTESQEEETTENSTLESLSGKKLTQKLKEDSEAESTESVPLVCKS
                                                                                                                                                                                                                                                                             924 GVEERTKSOKPLPKDKETNRNHSNSDNTETKDPAPQN--SNPAEEPRKPQKSGIMKQQRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Burnett, J. P.
APPLICANT: Mayne, Nancy G.
APPLICANT: Sharp, Robert L.
APPLICANT: Snyder, Yvone M.
TITLE OF INVENTION: EXCITATORY AMINO RECEPTOR PROTEIN AND
TITLE OF INVENTION: RELATED NUCLEIC ACID COMMONWARD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---FRDSVDSGSTTPNSPVSESALCIPSSPK 1164
                                                                                                                                                                                                                                                                                                                                                                                                                        982 NPTTANSDLNPGTTQMKDNFDIGEVCPWEVYDLTPGPVPSESK 1024
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PatentIn Release #1.0, Version #1.25
                                                                                                                                   880 ASAHNLSSEKKTGHPR-TSMLQKSLSVIASAKEKTLGLAG----
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18.6%; Pred. No. 2.6e-07;
tive 135; Mismatches 383
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APPLICATION NUMBER: US/08/282,853
FILING DATE:
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STREET: Lilly Corporate Center
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 ---MKVDINLQ 311
                                                                                                      443 KTNFTGVSGDTILFDENGDSPGRYEIMNFKEMG------KDYFDYINVGSWDNGEL 492
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                                                                     KVDIDQCSSDGWFSGTHKCHLNNSECMPIKGLGFVLGAYECICKAGFYHPGVLPVNNFRR
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NG-----SYKPGWLV-TLSSAIYGL---QPNLVPEFRGV---
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                                                                                                   APPLICANT: Daggett, Lorrie
APPLICANT: E111s, Steven B.
APPLICANT: Liaw, Chen
APPLICANT: Dontsler, Aaron
APPLICANT: Johnson, Edwin C.
APPLICANT: Hess, Stephen D.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF
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STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPALLAL
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,270
FILING DATE: 02-JUN-1994
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Best Local Similarity 18.5%; Pred. No. 5.7e-07;
Matches 207; Conservative 131; Mismatches 383;
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PELGATION 1433
PELGATION NUMBER: US 08/072,574
FILING DATE: 04-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: REJESTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: FP41 9772
TELECOMMUNICATION INFORMATION:
TELERAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 10:
                           Sequence 10, Application US/08486270 Patent No. 5807689 GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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APPLICANT: Liaw, Chen
APPLICANT: Pontsler, Aaron
APPLICANT: Johnson, Edwin C.
APPLICANT: Hess, Stephen D.
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF
CORRESPONDENCE ADDRESS:
                                             ---FLSRTAQRIPYMTGGRVMRMLAVILLVVFWFLIGWTSSVCQN
                                                                                                                                LGIIVALFIMEPPDIMHDYPSIREVYLICNTTNLGVVTPLGNNGLLILSCTFYAFKTRNV
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STREET: 444 South Flower Street, Suite 2000
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APPLICANT: Ellis, Steven B.
APPLICANT: Liaw, Chen
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                                                                                                                                         Version #1.25
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ilarity 18.5%; Pred. No. 5.7e-07;
Conservative 131; Mismatches 383;
                                                                                                                                                                    ELLING DATE: 02-JUN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/072,574
FILING DATE: 04-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stenhan
                                                                                                                                    SOFTWARE: Patentin Release #1.0,
                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                 NAME: Reiter, Stephen E. REGISTRATION NUMBER: 31,192
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LENGTH: 1212 amino acids
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                                                                                                                                                            CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                           COMPUTER READABLE FORM:
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FILING DATE: 04-JUN-1993
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Matches 207; Conserval
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 VPKVYIILAKPERNVRSAFTTSTVVRMHVGDGKSSSAASRSSSLVNLWKRRGSSGETLR- 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pontsler, Aaron
Johnson, Edwin C.
Hess, Stephen D.
TITLE OF INVENTION: HUMAN METABOTROPIC GLUTAMATE RECEPTORS,
NUCLEIC ACIDS ENCODING SAME AND USES THEREOF
                                                                                                                   TASSSNGKSVT-----
                            ELKKLYAQLEIYKRKKMITNNPHLQKKRCSKKGLGRSIMRRITEIPETVSRQCSKEDKEG
                                                                                      ADHGTAKGTALIRKNPPESSGNTGKSKEETLKNRVFSLKKSHSTYDHVRDQTEESSSLPT
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ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STREET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: CA
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APPLICATION NUMBER: US/08/486,270
FILING DATE: 02-JUN-1994
APPLICATION NUMBER: US 08/072,574
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APPLICATION NUMBER: US/09/153,757
FILING DATE: 15-Sep-1998
CLASSIFICATION: <UNMOWN>
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                   ----TPKG------SMGNGGRA-----
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Patent No. 6413764
GENERAL INFORMATION:
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Ellis, Steven B.
Liaw, Chen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        609 VVKSSSRELCYIILAGICLGYLCTFCLIAKPKQIYCYLQRIGIGLSPAMSYSALVTKTNR 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---FLSRTAQRIPYMTGGRVMRMLAVILLVVFWFLIGWTSSVCQN 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEKQISL-----IGQGKTSDHLIFNMCLIDRWDYMTAVA-EFLFLLWGVYLCYAVRTV 603
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PSAFHEPRYMAVAVHNELIISAIFHTIRFVLASRLQSDWMLMLYFAHTHLTVTVTIGLLL 663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1212;
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                                        NAME: Relter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: FP41 9772
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
TELEFAX: 619-546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 193.5;
Pred. No. 5.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 10: US-09-153-757-10
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SEQUENCE CHARACTERISTICS:
LENGTH: 1212 amino acids
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ATTORNEY/AGENT INFORMATION
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18.5%;
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                                                                                                                                                                                                                                                                             --TMTTFAEIQPLPAIEV 1123
  ---HPRTSMLQKSLSVIASAKEKTLGLAGKTQTAGVEERT 929
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                                                                                                                                                                                      NISELN-----SMMLSTAAP-----SPGVGAPLCSSYLIPKEIQL-----PT-
                                                                                                                                                                                                                                 SLKEKSHHKPKAAEVCQQSNQKRIDKAEVCLWESQGQSILEDEKLLISKTPVLPERAKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: Daggett, Lorrie

APPLICANT: Elia, Steven B.

APPLICANT: Liaw, Chen

APPLICANT: Liaw, Chen

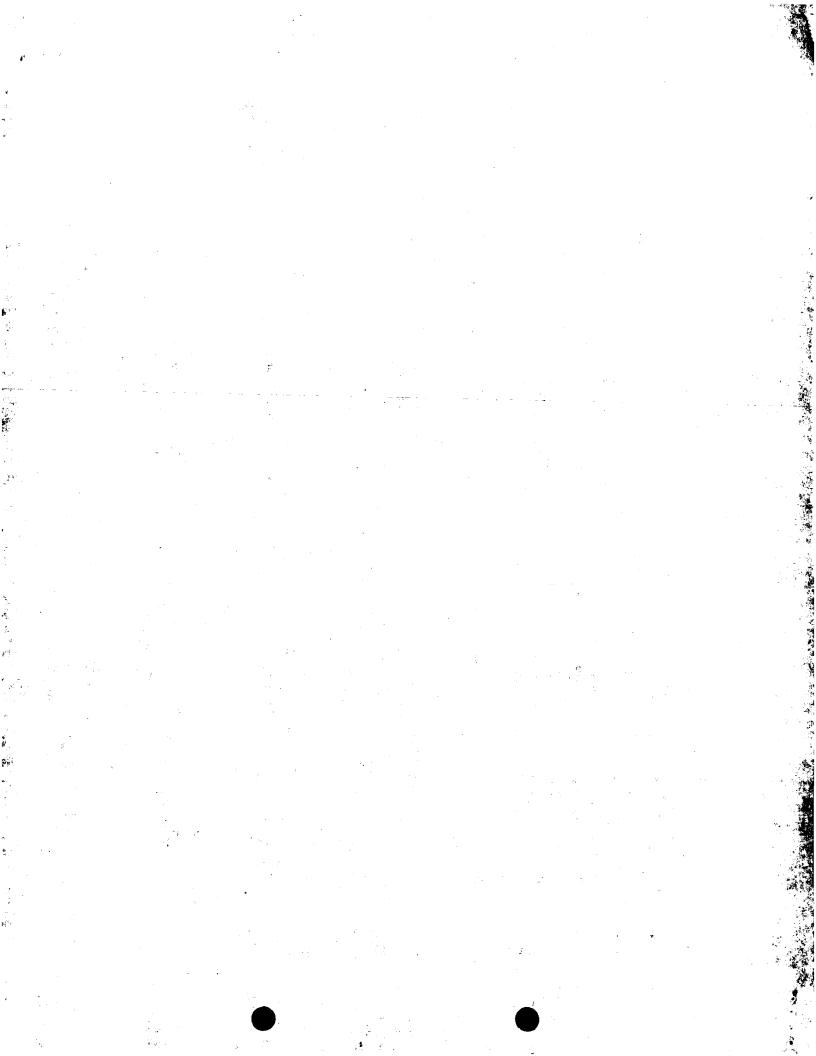
APPLICANT: HOWAN WATABOTROPIC GLUTAMATE RECEPTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING SAME AND USES THEREOF
NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                 1103 NGG-QPRAANVCAG----QSEELPPKAVASKTENENLNQIGHQEKKTSSSEENVRGSYNS
                                                                         KSQKPLPKDKETNRNHSNSDNTETKDPAPQ-NSNPAEEPRKPQKSGIMKQ--QRVNPTTA
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                                    GSAGGVGATGGAGCAGAGPGGPESPDAG -- PKALYDVAEAEEHFPAPA --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark STREET: 444 South Flower Street, Suite 2000 CITY: Los Angeles STATE: CA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.0%; Score 193; DB 1; Le
Best Local Similarity 18.8%; Pred. No. 6e-07;
Matches 177; Conservative 116; Mismatches 402;
                                                                                                                                                                                                                                                                                                                                                                                               SNNFQQPLTSRAEVCPWEFETPAQPNAGRSVALPAS 1193
                                                                                                                                                                                                                                                                                                                                                                                                                          ----TPNSPVSESALCIPSS 1194
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REGISTRATION NUMBER: 31,192
REFERENCE/POCKET NUMBER: P41 9383
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213-622-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/072,574
FILING DATE: 19930604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-072-574-8
; Sequence 8, Application US/08072574
; Patent No. 5521297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 8:
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LENGTH: 1180 amino acids
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CLASSIFICATION:
HNLSSEKKTG-
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1020 SSQGSLMEQISSVVTRFTANISELNSMMLSTAAPSPGVGAPLCSSYLIPKEIQLPTTMTT 1079
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932
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                                                                                                                          308 INLOKVDIDQCSSDGWFSGTHKCHLNNSECMPIKGLGFVLGAYECICKAGFYHPGVLPVN 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KTCNSSLTLKTHHVQDSKMGFVINAIYSMAYGLHNMQMSLCPGYAGLCDAMKPIDGRKLL
                                                                                                                                                  : | | : | | : | | : | : | : | ESLMKTNFTGVSGDIILFDENGDSPGRYEIMNFKEMG------KDYFDYINVGSWD
                                                                                                                                                                                                                             CPFC-----ADD-SPCFVQEDKYLR-----LAIISFQGLCMLLDFVSMLVVYHFRKAK
                                                                                                                                                                                                                                                                                                   609 VVKSSSRELCYIILAGICLGYLCTFCLIAKPKQIYCYLQRIGIGLSPAMSYSALVTKTNR
                                                                                                                                                                                                                                                                                                                                                                                                                          -----FLSRTAQRIPYMTGGRVMRMLAVILLVVFWFLIGWTSSVCQN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    879 NGKSVTWAQNEKSSRGQHLWQRLSIHINKKENPNQTAVIKPFPKSTESRGLGAG----
                                                     -----KPGWLV-TLSSAIYGL---QPNLVPEFRGV------MKVD
                                                                                                                                                                                                                                                                                                                                                 SIRASGLILLETILFGSLLLYFPVVILYFEPSTFRCILLRWARLLGFATVYGTVTLKLHR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEKQISL-----IGQGKTSDHLIFNMCLIDRWDYMTAVA-EFLFLLWGVYLCYAVRTV
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                                                                                                                                                                                                  NFRRRGPDQHI----SGSTKDVSEE-------AYVCLPCREG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NPTTANSDLNPGTTQMKDNFDIGEVCPWEVYDLTPGPVPSESK 1024
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6382
1 MGAWAYPLLLCLLLAQLGLG......LSANKIAGPRKEEIWDSFKV 1215
 5.1.3
Compugen Ltd.
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GenCore version Copyright (c) 1993 - 2003
                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                        score:
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Lotal number of hits satisfying chosen parameters: length: 0 length: 2000000000 imum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published\_Applications\_AA:\* Database

/ cgn2\_6/ptodata/1/pubpaa/USO8\_NEW\_PUB.pep:\*
/ cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
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/ cgn2\_6/ptodata/1/pubpaa/USO0\_PUBCOMB.pep:\* 55: 66: 110: 111: 14:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 2, Appli		Sequence 5, Appli	Sequence 4, Appli	356	Sequence 17, Appl	Sequence 34248, A	Sequence 4, Appli	Sequence 36182, A	Sequence 6, Appli	Sequence 4, Appli	Sequence 444, App	Sequence 12713, A	Sequence 3, Appli	Sequence 15, Appl	Sequence 4, Appli	Sequence 6, Appli	Sequence 988, App	
	ID	US-09-775-181-2	US-09-775-181-4	US-10-027-923-5	US-10-027-923-4	US-09-864-761-35612	US-09-924-154-17	US-09-864-761-34248	US-09-765-272-4	US-09-864-761-36182	0-966-838-60-SD	US-09-902-432-4	US-09-841-132-444	US-09-815-242-12713	US-09-738-877-3	US-09-924-154-15	US-09-734-672-4	US-09-982-828-6	US-09-925-299-988	US-09-902-432-2
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Sequence 11317, A Sequence 2816, App Sequence 1065, Ap Sequence 1065, Ap Sequence 1065, Ap Sequence 2, Appl Sequence 303, App Sequence 4, Appl Sequence 2, Appl Sequence 3, Appl	,
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### ALIGNMENTS

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           Sequence 2, Application US/09775181
Patent No. US20020038013A1
GENERAL INFORMATION:
APPLICANT: Donoho, Gregory
APPLICANT: Hilbun, Erin
TITLE OF INVENTION: No. US20020038013Alel Human Membrane Proteins and
TITLE OF INVENTION: Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0129-USA
CURRENT APPLICATION NUMBER: US/09/775,181
CURRENT FILING DATE: 2000-02-01
PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                            61 WSRSTDGTILAQKLAEEVPMDVASYLYTGDSHQLKRANCSGRYELAGLPGKWPALASAHP
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illarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity
Matches 1215; Conserv
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US-09-775-181-2
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GENERAL INFORMATION:

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                                  RGVMKVDINLQKVDIDQCSSDGWFSGTHKCHLNNSECMPIKGLGFVLGAYECICKAGFYH
                                                                  PGVLPVNNFRRRGPDQHISGSTKDVSEEAYVCLPCREGCPFCADDSPCFVQEDKYLRLAI
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Sequence 4, Application US/09775181 Patent No. US20020038013A1

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APPLICANT: Kamalaka Gulukota
APPLICANT: Yuhong Xie
APPLICANT: Janet Elizabeth Paulsen
TITLE OF INVENTION: NOVEL GLUTAMATE RECEPTOR MODULATORY PROTEINS AND
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APPLICANT: Donoho, Gregory
APPLICANT: Donoho, Gregory
APPLICANT: Donoho, Gregory
APPLICANT: Hilbun, Erin
TITLE OF INVENTION: NO US20020038013A1e1 Human Membrane Proteins
TITLE OF INVENTION: POLYMUCLEOLIDES Encoding the Same
FILE REPRENCE: LEX -0129-USA
CURRENT APPLICATION NUMBER: US/09/775,181
CURRENT FILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: US 60/180,414
NUMBER OF SEQ ID NOS: 5
SOTTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 1.2e-196;
2; Mismatches 2; I
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                                                                                                                                                                                                                                                        48.9%;
98.5%;
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Best Local Similarity 98.5
Matches 585; Conservative
                                                                                                                                                                                             TYPE: PRT
ORGANISM: Homo sapiens
US-09-775-181-4
                                                                                                                                                                                 LENGTH: 599
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APPLICANT: Yuhong Xie
APPLICANT: Janet Elizabeth Paulsen
TITLE OF INVENTION: NOVEL GLUTAMATE RECEPTOR MODULATORY PROTEINS AND
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND USES THEREFOR
FILE REFERENCE: GNN-024
CURRENT APPLICATION NUMBER: US/10/027,923
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/257,589
PRIOR FILING DATE: 2000-12-22
                                                                      1095 IPKEIQLPTMTFAE-----IQPLPAIEVT----GGAQGATGVSPAQETPTGAESAPGK
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Patent No. US20020142330A1
GENERAL INFORMATION:
APPLICANT: Briann Gaither Bates
APPLICANT: Kamalaka Gulukota
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SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                    3.3%; Score 211; DB 12; Length 1203; 18.7%; Pred. No. 1e-05;
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative 128; Mismatches 400;
                   FILE REFERENCE: GNN-024
CURRENT APPLICATION NUMBER: US/10/027,923
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/257,589
PRIOR FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Rattus sp. US-10-027-923-5
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Matches 179; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NG----
                                                                                                                                                                                                                                                                                 LENGTH: 1203
                                                                                                                                                                                                                                                                                                             TYPE: PRT
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1022 ----ESKVQKHVSIVASEMEKNPTFSLKEKSHHKPKAAEVCQQSNQKRIDKAEVCLWES 1076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           669 HSSNNPRDDIATEAYEDELDMGRSGSYLNSSINSAWSEHSLDPEDIRDELKKLYAQLEIY 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               729 KRKKMITNNPHLQKKRCSKKGLGRSIMRRITEIPETVSRQCSKEDKEGADHGTAKGTALI 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --KKHITPAPK-SKINCRKSTTGKS----TOTR---KSDKTG--RPLEKSMSTL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            789 RKNPPES-----SGNT-GKSKEETLKNRVFSLKKSHSTYDHVRDQTEESSSLPTES 838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QEEE------TTENSTLESLSGKKLTQKLKEDSEAESTESVPLVCKSASAHN 884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EKTEDSRTTVASDKLLTKTTKN-IQETISANELTQSLAEPTEHGG------RTANENN 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               941 TNRNHSNSDNTETKDPA-----PQNSNPAEEPRKPQKSGIMKQQRVNPTTANSDLNP 992
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N: EXPRESSED IN FETAL LIYER, SIGNAL = 2.4

N: EXPRESSED IN HERAL, SIGNAL = 0.98

N: EXPRESSED IN HEART, SIGNAL = 0.98

N: EXPRESSED IN BEART, SIGNAL = 1.5

N: EXPRESSED IN BONE MARROW, SIGNAL = 1.5

N: EXPRESSED IN LUNG, SIGNAL = 1.5

N: EXPRESSED IN ADULT LIYER, SIGNAL = 1.1

N: EXPRESSED IN ADULT LIYER, SIGNAL = 1.1

N: EXPRESSED IN AMBROOF, SIGNAL = 1.1

N: EXPRESSED IN AMBROOF, SIGNAL = 1.1

N: EXT. HUMAN HIT: AWB67076.1, EVALUE 1.00e-103

N: SYLIEMAN HIT: AWB67076.1, EVALUE 5.00e-63
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3.0%; Score 188.5; Db 10,
Best Local Similarity 22.1%; Pred. No. 0.00035;
Anismatches 242; Indels 155;
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00665
PRIOR APPLICATION NUMBER: PCT/USO1/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
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PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
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PRIOR FILING DATE: 2001-01-30
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PRIOR FILING DATE: 2000-06-31
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ORGANISM: Homo sapiens
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INFORMATION:
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LENGTH: 1325
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APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENDME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENDME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMBER: US 60/180,312

FILE REFERENCE: Acond.ca.X.1

CURRENT APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-09-03

PRIOR FILING DATE: 2000-09-04

PRIOR FILING DATE: 2000-09-04

PRIOR FILING DATE: 2001-01-04

PRIOR FILING DATE: 2001-01-30

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |------SMMLSTAAP-----SPGVGAPLCSSYLIPKEIQL------PT----- 1107
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               ---FSHSSNNPRDDIATE-AYEDELDMGRSGSYL--NSSINSAWSEHSLDPEDIRDELKK 720
                                                                                                                                                                                                                                                                                                                                                                       886
                                                                                                                                                                                                                                                                                                                                                                                                                              EKSSR------GOHLWORLSIHINKKENPNQTAVIKPFPKSTESRGLGAGAGGSAG 972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLPKDKETNRNHSNSDNTETKDPAPQ-NSNPAEEPRKPQKSGIMKQ--QRVNPTTAN-SD 989
                                                                                                                               LYAQLEIYKRKKMITNNPHLQKKRCSKKGLGRSIMRRITEIPETVSRQCSKEDKEGADHG
                                                                                                                                                                                                                                                781 TAKGTALIRKNPPESSGNTGKSKEETLKNRVFSLKKSHSTYDHVRDQTEESSSLPTESQE
                                                                                                                                                                                                                                                                                                                                                                       EETTENSTLESLSGKKLTQKL-----KEDSE-----AESTESVPLVCKSASAHNLS
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                                                                      YILLAKPERNVRSAFTTSTVVRMHVGDGKSSSAASRSSSLVNLWKRRGSSGETLR----
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---TPNSPVSESALCIPSS 1194
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APPLICATION NUMBER: PCT/US01/00664
FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00669
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Patent No. US20020048763A1
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332 LNNSECMPI---KGLGFVLGAYE--CIC-----KAGFYHPGVLPVNNFRRRGPDQHISG 380
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TKIF-DQLDKLFKERCSCMDTQVLEVKNKEMLSIDSNSEDATD-ISEKNGEEELYVNHNS 770
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APPLICANT: Sim, Kim L.

TITLE OF INVENTION: Anti-Plasmodium Compositions and Methods of UTILE OF INVENTION: Anti-Plasmodium Compositions and Methods of UTILE REFERENCE: 05213-0465 43170-262105
CURRENT APPLICATION WUMBER: US/09/924,154
CURRENT FILING DATE: 2001-08-07
PRIOR APPLICATION NUMBER: US 60/223,525
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
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Pred. No. 0.00057;
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Matches 182; Conservative 152; Mismatches 395;
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Patent No. US20020127241A1
GENERAL INFORMATION:
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18.2%;
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LENGTH: 1501
TYPE: PRT
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## Patent No. US20020048763A1

GENERAL INROPARATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Penn, Sharron G.

APPLICANT: Bank, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Chen, Wensheng

ITILE OF INVENTION: HUANN GENME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USFUL FO

ITILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE: Acomica -x-1

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PLILNG DATE: 2000-06-03

PRIOR PLILNG DATE: 2000-09-03

PRIOR PLILNG DATE: 2000-09-03

PRIOR PLILNG DATE: 2000-01-03-0

PRIOR PLILNG DATE: 2001-01-30

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Patent No. US20020048763A1
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                                                                                                                                                                                                 817
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817 SHSTYDHVRDQTEESSSLPTESQEEETTENSTLESLSGKKLTQKLKEDSE-----AES 869
                                                                                                                                                                      1162 QQPLTSRAEVCPWEFETPAQPNAGR 1186
                                                                                                                                                                                                                   1318 ERELQEAAAV-----PTTPRRGR 1335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/09765272 Patent No. US20020061545Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 571 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 19.8%
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE
                                                                                                                                                                                                                                                                                                                 US-09-765-272-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1049 PLVTEEKTVEPATVSEEAKPASEPAPAPVEQLEQVDLPPGADPDKEAAMMPAGVEEGSSG 1108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1109 DQPPYLDAKPPTPGASFSQAESNVDPEPDSTQPLSKP--AQKSEEANEPKAEKPDATADA 1166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NPGTTQMKDNFDIGEVCPWEVYDLTPGPVPSESKVQKHVSIVASEMEKNPTFSLKEKSHH 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPDANOKA------EAAPESQPPASE-----DLEVDPPVAAKDKKPN 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1051 KPKAAEVCQQSNQKRIDKAEVCLWESQGQSILEDEKLLISKTP-----VLPERAKEENGG 1105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --SGKKLTQKLKEDS 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          932 QKPLPKD-KETNRNHSNSDNTETKDPAPQNSNPAEEPRKPQKSGIMKQQRVNPTTANSDL 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSNNPRDDIATEAYEDELDMGRSGSYLNSSINSAWSEHSLDPED-IRDELKKLYAQLE- 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            727 ----IYKRKKMITNNPHLQKKRCSKKGLGRSIMRRITEIPETVSRQCSKEDKEGADHGTA 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        783 KGTALIRKNPPESSGNTGK-----SKEETLKNRVFSLKKSHST-----YDHVRD 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    932 KEEDSDFISGRIYGKQTSEGANSTTDSIQEPVVLFHSRFMELTRMQQKEKEKDQKPKEVE 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    812 NKFYSFALDKTITPDTKALLERAKSLSSSREENWSFLDWDSRFANFRNNKDKEKVDSAPR 871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EAESTESVPLVCKSASAHNLSSEKKT----GHPRTSMLQKSLSVIASAKEKTLG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 2665,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXPRESSED IN HEL100, SIGNAL - 7.7
EXPRESSED IN BT474, SIGNAL - 12
EST_HUMAN HIT: AU117052.1, EVALUE 0.00e+00
SWISSPROT HIT: P08640, EVALUE 3.00e-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.8%; Score 179.5; DB 10; Length 20.8%; Pred. No. 0.0037; tive 78; Mismatches 250; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : EXPRESSED IN FETAL LIVER, SIGNAL = 8:5
: EXPRESSED IN ADULT LIVER, SIGNAL = 4:6
: EXPRESSED IN PLACENTA, SIGNAL = 14
: EXPRESSED IN HEART, SIGNAL = 7:2
: EXPRESSED IN HEART, SIGNAL = 9:5
: EXPRESSED IN HELA, SIGNAL = 9:5
: EXPRESSED IN HELA, SIGNAL = 7:1
: EXPRESSED IN LUNG, SIGNAL = 9:3
                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 34248
              PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR PELING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2000-09-21
PRIOR PELICATION NUMBER: US 60/234,687
PRIOR PELING DATE: 2000-09-21
PRIOR PELING DATE: 2000-06-30
PCT/US01/00663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              916 -LAGKTQT-----
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TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
                                                          1259 TRTASKNSAADLEHPEPSLPLSRTRRRNVRSVYATMGDHENR-SPVKEPVEQPRVTRKRL 1317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 SNQKSSVATPTKQQKVDYNVTPNFVDHPSTVQAIQEQTPVSSTKPTEVQVVEKPFSTELI 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
1106 QPRAANVCAGQSEELPPKAVASKTENENLNQI----GHQEKKTSSSEENVRGSYNSSNNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          672 NNPRDDIATEAYEDELDMGRSGSYLN----SSINSAWSEHSLDPEDI-
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; Mismatches 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.8%; Score 178; DB 10; 19.8%; Pred. No. 0.00053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Human Genome Sciences, Inc. STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.
SOFTWARE: ASCIT Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/765,272
FILING DATE: 22-Jan-2001
CLASSIFICATION: <u >Unknown></u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: PB340P2 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/961,083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Brookes, A Anders
REGISTRATION NUMBER: 36,373
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971 QKS-GIMKQQRVNPTTANSDLNPGTTQMKDNFDIGEVCPWEVYDLTPGPVPSESKVQKHV 1029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EENVRGSYNSSNNFQQPLTSRAEVCPWEFETP---AQPNAGRSVALPASSALSANKIAGP 1204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 SPAEAKSPEKEEAKSPAEVKSPEKAKSPAKEEAKSPPEAKSPEKEEAKSPAEVKSPEKAK 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          859 QKLKEDSEAESTESVPLVCKSASAHNLSSEKKTGHPRTSMLQKSLSVIA--SAKEKTLGL 916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    917 AGKTQTAGVEER-----TKSQKPLPKDKETNRNHSNSDNTETKDPAPQNSNPAEEPRKP 970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      334 KSPVKEEAKSPE---KAKSPEKAKTLDV--KSPEAKTPAKE----EARSPADKFPEK--- 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           754 IMRRITEIPETVSRQCSKEDKEGADHGTAKGTALIRKNPP-ESSGNTGKSKEETLKNRVF 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              382 AKSPVKEEVKSPEKAKSPLKADAKAPE-KEIPKKEEVKSPVKEEEKPQEVKVKEPPKKAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183 SPAKEEAKSPAEAKSPEKAKSPVKEEAKSPAEAKSPVKEEAKSPAEVKSPEKAKSPTKEE
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                                                                                                                                                                                                                                                                                                                                         N: MAP TO AC005529.7

N: EXPRESSED IN HELA, SIGNAL = 1.3

N: EXPRESSED IN HELAO, SIGNAL = 0.94

N: EXPRESSED IN HEART, SIGNAL = 1.3

N: EXPRESSED IN FEAL LIVER, SIGNAL = 1.3

N: EXPRESSED IN BRAIN, SIGNAL = 5.6

N: SWISSPROT HIT: P12036, EVALUE 2.00e-33

N: EST_HUMAN HIT: BF445754.1, EVALUE 3.00e-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SED ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 36182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.7%; Score 174; DB 10;
20.6%; Pred. No. 0.0011;
vative 79; Mismatches 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/09839996
Publication No. US20030009010A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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Best Local Similarity
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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
                                                                                                                                                                                                                                                                                                                                                                                                                              VOKHVSIVASEMEKNPTFSLKEKSHHKPKAAEVCQQSNQKRIDKAEVCLWES--QGQSIL 1082
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                                                                                                                                                                                                                                                                                                               EEPRKPQKSGIMKQQRVNPTTANSDLNPGTTQMKDNFDIGEVCPWEVYDLTPGPVPSESK 1024
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                                                                                           ----RISMLQKSLSVIASAKEKTL 914
  GLAGKTQTAGVEERTKSQKPLPKDKETNRNHSNSDNTETKDPAPQNSN------PA
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CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR PEDLICATION NUMBER: US 60/180,312
PRIOR PELLING DATE: 2000-02-04
PRIOR PELLING DATE: 2000-05-26
PRIOR PELLING DATE: 2000-06-26
PRIOR PELLING DATE: 2000-06-26
PRIOR PELLING DATE: 2000-06-26
PRIOR PELLING DATE: 2000-01-03
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PELLING DATE: 2000-10-04
PRIOR PELLING DATE: 2001-01-04
PRIOR PELLING DATE: 2001-01-04
PRIOR PELLING DATE: 2001-01-13
PRIOR PELLING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
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Patent No. US20020048763A1
                                                                                        870 TESVPLVCKSASAHNLSSEKKTGHP---
        EEVS----REIVSTSTTAPSPRIVEK-
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US-09-864-761-36182
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TYPE: PRT ORGANISM: Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      189;
               ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1848;
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                                                                                                                                                   COMPUTER: IBM PC remartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                     NAME: Trecartin, Richard F.
REGISTRATION NUMBER: 31,801
REFERENCE/DOCKET NUMBER: a-59941/RFT/RMS
TELECOMMUNICATION INFORMATION:
TELEFAX: (415,781-1989
TELEFAX: (415,398-3249
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18.4%; Pred. No. 0.012;
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                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/839,996
FILING DATE: 20-Apr-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                    APPLICATION WIBER: US/08/296,791
FILING DATE: 25-AUG-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1848 amino acids
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                                                                 STATE: California
COUNTRY: United States
ZIP: 94111-4187
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
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Best Local Similarity
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1070 EVCLWESQGQSILEDEKLLISKTPVLPE---RAKEENGGQPRAANVCAGQSEELPPKAVA 1126
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Best Local Similarity 22.1%; Pred. No. 0.019;
Matches 135; Conservative 101; Mismatches 257;
                                                                                                                                                                                                                                                                                                                                                                                                                       1169 AEVCPWEFETPAQPNAGRSVALPASSALSANKIA 1202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Jaken
TITLE OF INVENTION: TUMOR SUPPRESSOR GENE
FILE REFERENCE: A30528 A-FWC-A 070156.0597
CURRENT APPLICATION NUMBER: US/09/902,432
CURRENT FILING DATE: 1202-04-08
PRIOR APPLICATION NUMBER: 08/978,277
PRIOR APPLICATION NUMBER: 08/65,401
PRIOR APPLICATION NUMBER: 08/65,401
PRIOR APPLICATION NUMBER: 08/65,401
PRIOR APPLICATION NUMBER: 08/65,121
PRIOR APPLICATION NUMBER: 08/655,121
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1037 EKNPTFSLKEKSHHKPKAAEVCQQSNQKRIDKAEVCLWESQGQSILEDEKLLISKTPVLP 1096
                                                                                                                                                                                                      1156 NSSNNFQQPLTSRAEVCPWEFETPAQPNAG 1185
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/191, 078
PRIOR FILING DATE: 2000-03-21
PRIOR PELLING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/26/
PRIOR APPLICATION NUMBER: 60/25/
PRIOR PELING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/25/,931
PRIOR FILING DATE: 2000-12
PRIOR APPLICATION NUMBER: 60/25/,931
PRIOR FILING DATE: 2000-12
PRIOR FILING DATE: 2000-12-2
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APPLICANT: Ohlsen, Kari L.
AAPPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
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Carr, Grant J.
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US-09-815-242-12713
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LENGTH: 2344
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1043 SLKEKSHHKPKAAEVCQQSNQKRIDKAEVCLWESQGQSILEDEKLLISKTPVLPERAKEE 1102
                                                                                      1103 NGGQPRAANVCAGQSEELPPKAVASKTEN--ENLNQIGHQEKKTSSSEENVRGSYNSSNN 1160
                                                                                                                                                                             1161 FQ------QPLTSRAE---VCPWE----FETPAQPNAGR-SVALPASSALSANKIAG 1203
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                                                                                                                317 KSLTITGITGTIDEVSNIATDSGAGVFTKENLSCTNTNSLQFLKNSAGQHG-GGAYVTQT 375
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                            376 MSVTNTTSESITTPPLIGEVIFSENTAKGHGGGICTNKLSLSNLKTVTLTKNSAKESGGA
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APPLICANT: SKEIKY, Yasir A.W.
APPLICANT: Probst, Peter
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C8
CURRENT APPLICATION NUMBER: US/09/841,132
CURRENT FILING DATE: 2001-04-23
NUMBER OF SEQ ID NOS: 599
SOFTWARE: FastSEQ for Windows Version 3.0/4.0
SEQ ID NO 444
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                                                                                                                                                                                                                                                                                                                781 PSREESWVSIK 791
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US-09-841-132-444
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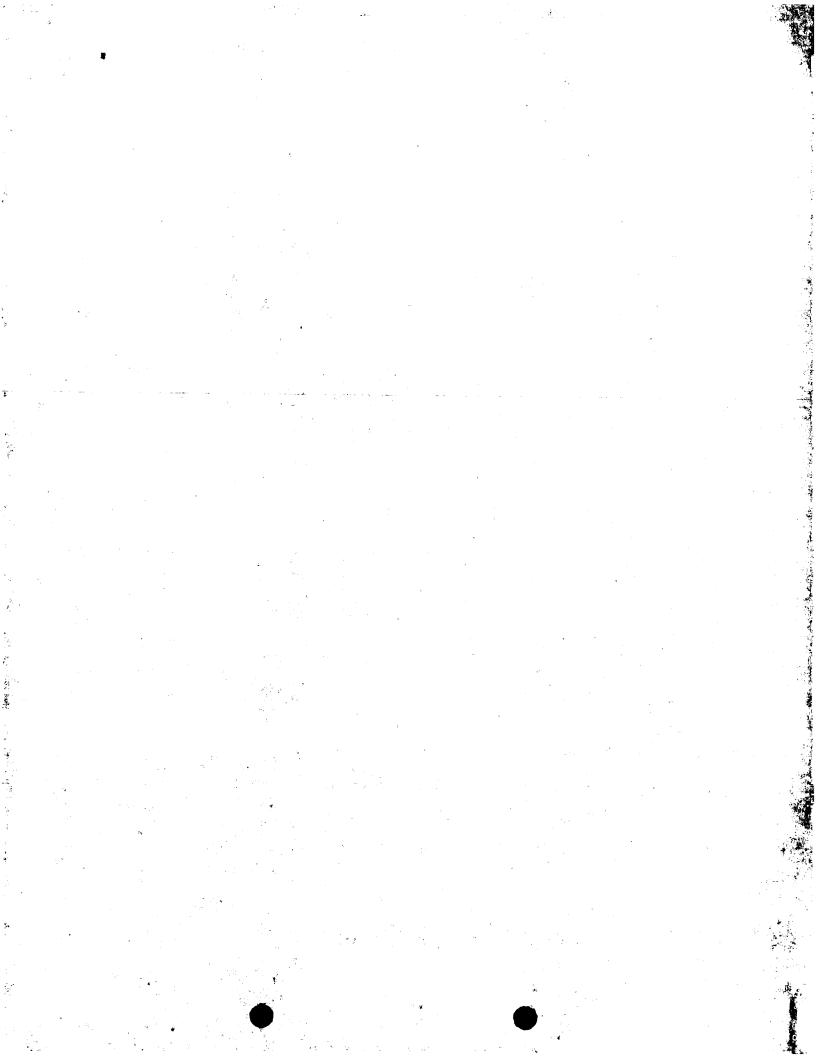
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691 NTLPNSNIDQSNENTDESSD----SHTEEITDESVSSSESGSSTPQDGGAASSGAP---
                                                                                                                                                                                                                                                                                                                    ERAKEENGGQPRAANVCAGQSEELPPKAVASKTENENL-NQIGHQEKKTSSSEENVRGSY
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TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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163.5; DB 10; Best Local Similarity 17.6%; Pred. No. 0.034; Matches 104; Conservative 100; Mismatches 271;
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1090 SKTPVLPERAKEENGGQPRAANVCAGQSEELPPKAVASKTENENLNQIGHQE-KKTSSSE 1148
                                                                                                                                                                                                   988 SDLNPGTTQMKDNFDIGEVCPWEVYDLT-----PGPVPSESKVQKHVSIVASEMEKN 1039
                                                                                                                                                                                                                                                                                                  1040 PTFSLKEKSHHKPKAAEVCQQSNQKRID------KAEVCLWESQGQSILEDEKLLI 1089
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                                                                                                                                                                                                                                                                                                                                                   887 QVHMMAAAVADGTRAATIIEERSPSWISASVTEPLEQVEAEAALLT---EEVLEREVIAE 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                   944 EEPPTVTEPLPENR - - EARGDTVVS - - EAELTPEAV - - - TAAETAGPLGSEEGTEASAAE 996
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  -TNRNHSNSDNT
                                                717 GKDKETGTDGILAGSQEHDPGQGSSSPEQAGSPTEGEGVSTWESFKRLVTPRKKSKSKLE
                                                                                                    --RKPQKSGIMKQQRV---NPTTAN
                                                                                                                                        777 EKSEDSIAGSGVEHSTPDTEPGKEESWVSIKKFIPGRRKKRPDGKQEQAPVEDAGPTGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Narum, David L.
APPLICANT: Sim, Kim L.
TITLE OF INVENTION: Anti-Plasmodium Compositions and Methods of Use
FILE REPRENCE: 05213-0465 43170-262105
CURRENT APPLICATION NUMBER: US/09/924,154
CURRENT FILING DATE: 2001-08-07
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 17
SOFWARE: Patentin version 3.1
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21.0%; Pred. No. 0.018;
tive 75; Mismatches 209;
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  909 AKEKTLG----LAGKTQ-TAGVEERTKSQKPLPKDKE-
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Patent No. US20020127241A1
GENERAL INFORMATION:
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Matches 111; Conservative
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ORGANISM: Mammalian
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APPLICANT: Watson, Susan
APPLICANT: Glynne, Richard
TITLE OF INVENTION: SCREENING FOR ANGIOGENESIS, COMPOSITIONS, AND MET
TITLE OF INVENTION: SCREENING FOR ANGIOGENESIS MODULATORS
TITLE REPERENCE: A-69806/DJB/JJD
CURRENT APPLICATION NUMBER: US 09/637,977
PRIOR FILING DATE: 2000-08-11
PRIOR FILING DATE: 1099-08-11
PRIOR APPLICATION NUMBER: US 60/148,425
PRIOR FILING DATE: 1099-08-11
PRIOR FILING DATE: 2000-08-11
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                                                                                                                                                                                                   QRVNPTTANSDLNPGTTQMKDNFDIGEVCPWEVYDLTPGPVPSESKVQKHVSIVASEMEK 1038
                                                                                                                                                                                                                                                                                                NPTFSLKE----KSHHKPKAAEVCQQSNQKRIDKAEVCLWESQGQSILEDEKLLISKTP 1093
  -SLSVIASAKEKT---LGLAG 918
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                                                                                                 919 KTQTAGVEERTKSQKPLPKDKETNRNHSNSDNTETKDPAPQNSNPAEEPRKPQKSGIMKQ
                                                                                                                                                                                                                                                  ----TSTSTSLSDSTSISKSTSQSGSTST----SASLSGSESESDSQSISTSTSESKSE
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; Pred. No. 0.029;
83; Mismatches 232; Indels 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1152 RGSYNSSNNFQQPLTSRAEVCPWEFETPAQPNAGRSVALPASSALSANKI 1201
                                                                                                                                   SMNQSGVDSNSASQS---ASTSTSTSTSESDSQSTSSYTSQSTSGSES---
  STESVPLVCKSASAHNLSSEKKTGHPRTSMLQK--
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Best Local Similarity 21.5%;
Matches 124; Conservative 8
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US-09-738-877-3
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3199
1 MGAMAYPLLICLLLAQLGLG......YMTAVGMWSLVSYDGLTIFQ 599
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

2			Description	Human G-protein co	Human G-protein co	Drosophila melanog	Drosophila G-prote	Drosophila melanog	Drosophila melanog	Drosophila melanog	Human calcium sens	Chimeric hCAR/hmGl	Chimeric human hCA
COLUMNIA			ID	AAE06643	AAE06642	ABB70858	AAU38983	ABB67185	ABB65498	ABB69976	AAY45000	AAY49126	AA015092
			DB	22	22	22	22	22	22	22	21	20	23
			Length	599	1215	699	699	176	976	1677	974	917	917
	ФP	Query	e Match Length DB I	100.0	97.5	10.6	10.6	7.5	5.0	4.7	4.4	4.4	4.4
			Score	3199	3119.5	339	339	238.5	161.5	149	141.5	139.5	139.5
		Result	No.		7	3	4	5	9	7	89	6	10

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#### ALIGNMENTS

Human; G-protein coupled receptor; NGPCR; gene therapy; cancer; diabetes; inflammation; immune disorder; heart disease; obesity; coronary disease; metabolic disorder; physiological disorder; therapeutic; drug screening; signal transduction; behavioural disorder. Novel isolated polynucleotides encoding human G protein coupled Human G-protein coupled receptor (NGPCR) #2 AAE06643 standard; Protein; 599 AA (LEXI-) LEXICON GENETICS INC. 04-FEB-2000; 2000US-0180414 01-FEB-2001; 2001WO-US03648 (first entry) WPI; 2001-488870/53. N-PSDB; AAD12293. Donoho G, Hilbun E; WO200157086-A2, 16-OCT-2001 Homo sapiens 09-AUG-2001. AAE06643; RESULT 1 

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tor (NGPCR), useful as probe and for treating disease involving detecting mutant NGPCR or abnormally expressed NGPCRs for
   receptor (NGPCR), useful
                                                                               diagnosing disease
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Claim 4; Page 70-71; 73pp; English.

The present sequence is human G-protein coupled receptor (NGPCR) which is a 7 transmembrane protein of G-protein coupled receptor (GPCR) super family. NGPCR is expressed in hypothalamus, foetal brain, brain, cerebellum and testis. NGPCR spans the cellular membrane and is involved in signal transduction pathways. Human NGPCR is useful for treating obesity, inflammation, immune disorders, diabetes, heart and coronary disease, metabolic disorders and cancer. NGPCR's are also used as reagents in assays for screening compounds that are useful in the therapeutic treatment of physiological and behavioural disorders. NGPCR is useful for identifying compounds that modulate NGPCR gene expression and/or gene product activity. NGPCR NDA is also useful for the diagnostic and prognostic evaluation of disorders related to NGPCR function. Nucleotide constructs encoding functional NGPCR and mutant NGPCR variants are used in gene therapy. NGPCR probes are also useful for the identification, selection and validation of novel molecular targets for drug discovery

599 AA; Sequence

SSXS

; 0 240 240 300 WSRSTDGTILAQKLAEEVPMDVASYLYTGDSHQLKRANCSGRYELAGLPGKWPALASAHP 120 SLHRALDTLTHATNFLNVMLQSNKSREQNLQDDLDWYQALVWSLLEGEPSISRAAITFST 180 Gaps 9 1 MGAMAYPLLLCLLLAQLGLGAVGASRDPQGRPDSPRERTPKGKPHAQQPGRASASDSSAP 60 DSLSAPAPQVFLQATREESRILLQDLSSSAPHLANATLETEWFHGLRRKWRPHLHRRGPN SLHRALDTLTHATNFLNVMLQSNKSREQNLQDDLDWYQALVWSLLEGEPSISRAAITFST ö Length 599; Indels 9.1e-300; ö DB Mismatches Score 3199; Pred. No. 9. ö 100.0%; Query Match 100. Best Local Similarity 100. Matches 599; Conservative 61 61 121 121 181 181 셤 ò g ò g ò g

RGVMKVDINLQKVDIDQCSSDGWFSGTHKCHLNNSECMPIKGLGFVLGAYECICKAGFYH QGPRGLGHSWRRKDGLGGDKSHFKWSPPYLECENGSYKPGWLVTLSSAIYGLQPNLVPEF 241 241 301 ò

300 360

RGVMKVDINLQKVDIDQCSSDGWFSGTHKCHLNNSECMPIKGLGFVLGAYECICKAGFYH 360 PGVLPVNNFRRRGPDQHISGSTKDVSEEAYVCLPCREGCPFCADDSPCFVQEDKYLRLAI 420 301 361 pp ò

361

P ò qq CILLRWARLLGFATVYGTVTLKLHRVLKVFLSRTAQRIPYMTGGRVMRMLAVILLVVFWF 540 481 δ g

599 541 LIGWTSSVCQNLEKQISLIGQGKTSDHLIFNMCLIDRWDYMTAVGMWSLVSYDGLTIFQ 541 ò ద

AAE06642; 

(first entry) 16-OCT-2001 Human G-protein coupled receptor (NGPCR) #1.

Human; G-protein coupled receptor; NGPCR; gene therapy; cancer; diabetes; inflammation; immune disorder; heart disease; obesity; coronary disease; metabolic disorder; physiological disorder; therapeutic; drug screening; signal transduction; behavioural disorder.

Homo sapiens.

WO200157086-A2

09-AUG-2001

01-FEB-2001; 2001WO-US03648.

04-FEB-2000; 2000US-0180414.

(LEXI-) LEXICON GENETICS INC

Donoho G, Hilbun E;

WPI; 2001-488870/53. N-PSDB; AAD12292 Novel isolated polynucleotides encoding human G protein coupled receptor (NGPCR), useful as probe and for treating disease involving GPCR, detecting mutant NGPCR or abnormally expressed NGPCRs for

Claim 2; Page 66-69; 73pp; English.

diagnosing disease

The present sequence is human G-protein coupled receptor (NGPCR) which is a 7 transmembrane protein of G-protein coupled receptor (GPCR) super family. NGPCR is expressed in hypothalamus, feetal brain, brain, cerebellum and testis. NGPCR spans the cellular membrane and is involved in signal transduction pathways. Human NGPCR is useful for treating obesity, inflammation, immune disorders, diabetes, heart and coronary disease, metabolic disorders and cancer. NGPCR's are also used as reagents in assays for screening compounds that are useful in the therapeutic treatment of physiological and behavioural disorders. NGPCR is useful for identifying compounds that modulate NGPCR gene expression and/or gene product activity. NGPCR DNA is also useful for the diagnostic and prognostic evaluation of disorders related to NGPCR function. Nucleotide constructs encoding functional NGPCR and mutant NGPCR variants are used in gene therapy. NGPCR probes are also useful for the identification, selection and validation of novel molecular targets for drug discovery.

1215 AA; Sequence

Gaps Length 1215; Score 3119.5; DB 22; Pred. No. 1.3e-291; 2; Mismatches 2; Ir 97.5%; 98.5%; Best Local Similarity 98.5 Matches 585; Conservative Query Match

1;

1 MGAMAYPLLLCLLLAQLGLGAVGASRDPQGRPDSPRERTPKGKPHAQQPGRASASDSSAP 60 QQ δ

WSRSTDGTILAQKLAEEVPMDVASYLYTGDSHQLKRANCSGRYELAGLPGKWPALASAHP 120 61 61 δ g

SLHRALDTLTHATNFLNVMLQSNKSREQNLQDDLDWYQALVWSLLEGEPSISRAAITFST 180 121 ò

121

g

DSLSAPAPQVFLQATREESRILLQDLSSSAPHLANATLETEWFHGLRRKWRPHLHRRGPN 240 181 ò

RESULT 2 AAE06642

AAE06642 standard; Protein; 1215

Gaps

98;

337 187 394 237 447 507 357

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specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                           110 GKWPALASAHPSLHRALDTLTHATNFLNVMLQSNKSREQNLQDDLDWYQALVWSLLEGEP 169
                                                                                                                                                                                                        --TRAEVSRRANGIAS-----YALNEDDNLLAFAIAAPSIHTVVVKFRDNVTIPPDQV
                                                                                                                                                                                                                                                                                                                         140 WPFRISFS-----EHR-IKVVAAAFIAADEDVC-NDGLEEVFGRRHGCDRNTTFC
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LLTENKPAATRDVYTCLCRESYYLPN-STLOGFR------GDRVELSEGYDNYSCIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 GKWPC-RMFYDYTDIAEDAARQFIEFL----SGKFPNANTPIAID-----EP
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                                                                                                                                                                                                                                                                                               WLVTLSSAIYGLQPNLVPEFRGVMKVDINLQKVDIDQCSSDGW---FSGTHKCHLNNSEC
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2.4e-23;
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18-JUL-2000; 2000US-0618893.
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                                                                                               RGVMKVDINLQKVDIDQCSSDGWFSGTHKCHLNNSECMPIKGLGFVLGAYECICKAGFYH
                                                                                                                                                     ISFQGLCMLLDFVSMLVVYHFRKAKSIRASGLILLETILFGSLLLYFPVVILYFEPSTFR
                                                                                                                                                                                                           CILLRWARLLGFATVYGTVTLKLHRVLKVFLSRTAQRIPYMTGGRVMRMLAVILLVVFWF
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N-PSDB; ABL11288
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                                                              WO200171042-A2
             pharmaceutical
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ABB65498
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                                                                                                                       The invention relates to sixty six novel isolated Drosophila melanogaster G-protein coupled receptors (GPCR). The GPCR proteins and nucleic acids are useful in the treatment and diagnosis of GPCR-related conditions. The GPCR proteins and nucleic acids are also useful for identifying modulators of GPCR proteins for use as insecticides. The expression products such as mRNA, AAU38923. AAU38988 represent D. melanogaster G-coupled protein receptor amino acid sequences of
                                                                                                                                                                                                                                                                                                                                110 GKWPALASAHPSLHRALDTLTHATNFLNVMLQSNKSREQNLQDDLDWYQALVWSLLEGEP 169
                                                                                                                                                                                                                                                                                                                                                                                  170 SISRAAITFSTDSLSAPAPQVFLQATREESRILLQDLSSSAPHLA-----NATLETEWF 223
                                                                                                                                                                                                                                                                                                                                                                                                                                     280
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                                              Sixty six Drosophila Melanogaster G-protein coupled receptors (GPCR). useful in the treatment and diagnosis of GPCR-related conditions and for identifying GPCR modulators for use as insecticides -
                                                                                                                                                                                                                                                                                                                                                         GKWPC-RMFYDYTDIAEDAARQFIEFL----SGKFPNANTPIAID------EP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      140 WPFRISFS-----EHR-IKVVAAAFIAADEDVC-NDGLEEVFGRRHGCDRNTTFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLTENKPAATRDVYTCLCRESYYLPN-STLOGFR------GDRVELSEGYDNYSCIP
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                                                                                                                                                                                                                                                                                                                                                                                                         --TRAEVSRRANGIAS-----YALNEDDNILLAFAIAAPSIHTVVVKFRDNVTIPPDQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WLVTLSSAIYGLQPNLVPEFRGVMKVDINLQKVDIDQCSSDGW---FSGTHKCHLNNSEC
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                                                                                                                                                                                                                                                                                                         98;
                                                                                                                                                                                                                                                                               Length 669;
                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                      71; Mismatches 200;
                                                                                                                                                                                                                                                                                DB 22;
                                                                                                                                                                                                                                                                               10.6%; Score 339; DB 22 25.6%; Pred. No. 2.4e-23
                                                                                                  Claim 1; Page 275-277; 392pp; English.
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          WPI; 2001-616405/71.
N-PSDB; AAS57192, AAS57193.
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                                                                                                                                                                                                                                                       699
                                                                                                                                                                                                                               the invention.
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                                                                                                                                                                                                                                                       Sequence
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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Drosophila; developmental biology; cell signalling; insecticide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ID NO 28347; 21pp + Sequence Listing;
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Pred. No. 1.6e-14;
5; Mismatches 55;
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31.5%; Pre
tive 25;
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                                                                                                                                                                                                                                                                                 23-MAR-2001; 2001WO-US09231
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11-JUL-2000; 2000US-0614150
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genes from Drosophila and
interactions -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adams M,
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                                                                                                                                                                                                                                                                                                                                                                                                                        detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            400 CDDSYRLSEKVGYEQESKTQFVVDAVYAFAYALHNLHNDRCNTQSDQTTETRKHLQSESV 459
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 23286; 21pp + Sequence Listing; English
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llarity 20.1%; Pred. No. 6.2e-06;
Conservative 80; Mismatches 179;
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                                                                                                      2001WO-US09231
                                                                                                                                                       2000US-191637P
                                                                                                                                                                                   2000US-0614150
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                                                                                                                                                                                                                                                                                         Venter JC, Adams M,
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Matches 101; Conserv
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WO200171042-A2
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                                                                                                   23-MAR-2001;
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                                                 27-SEP-2001
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention issell in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detection reagent for detecting 1000 or more for elucidating cell signalling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WSPPYLECENGSYKPGWLVTLSSAI ----YGLQPNLVPEFRGVMKVDINLQKVDIDQCS 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --FSGTHKCHLNNSE 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AEPYPFGSRRQKMQQLQTHNRLGARRSLFLGSRMGAIDESTINDLQAFHSSHKCH--RTS 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  205 MVPVKRLNRKIKEPVSPKLSANQNVTPTRRIKRINTPVAVDPSPSPSVVARRARTSAALK 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                        developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 36720; 21pp + Sequence Listing; English.
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                                                                                                                                                                            Drosophila melanogaster polypeptide SEQ ID NO 36720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 149; DB 22;
Pred. No. 0.00023;
; Mismatches 83;
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                                                                                        AA.
SQVVITTSLIAIQVLITMIWMVV 759
                                                                                      ABB69976 standard; Protein; 1677
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14.38, Fr.,
37;
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11-JUL-2000; 2000US-0614150.
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genes from Drosophila and
interactions -
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                                                                                                                                                                                                                                                    Drosophila melanogaster
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Best Local Similarity
Matches 58; Conserv
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                                                                                                                                               26-MAR-2002
                                                                                                                                                                                                        Drosophila;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter JC,
                                                                                                                   ABB69976;
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SHIPSTIAVVGATGSGVSTAVANLLGLEYI-----POVSYASSS--RLLSNKNOFKS 182
                                                                                                                     | : | : | : | : | : | : | 3 | 440 RDCLAGTRKGIIEGEPTCCFECVECPDGEYSDETDASACNKCPDDFWSNENHTSCIAKEI 499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEO SSLFFIGEPQDWTCRLRQPAFGISFVLCISCILVKTNRVLLVFBAKIPTSFHRKWWGLNL 619
  AEEVPMDVASYLYTGDSHQLKRANCSGRYELAGLPGKWPALASAHPSLHRALDTLTHATN 134
                                                                                                                                                                                 187 APQVFLQATREESRILLQDLSSSAPHLANATLETEWFHGLRRKWRPHLHRRGPNQGP--- 243
                                                                                                                                                                                                                           ---IVVFSSGPDLEPLIK 281
                                                                                                                                                                                                                                                                       ----RGL-GHSWRRKDGLGGDKSHFKWS-----PPYLECENGSYKPGWLVTLSSAIYG 291
                                                                                                                                                                                                                                                                                                                  282 EIVRRNITGKIWLASEA------WASSSLIAMPQYFHVVGGTIG-----FA 321
                                                                                                                                                                                                                                                                                                                                                                292 LQPNLVPEFRGVMKVDINLQKVDIDQCSSDGWFSGTHKCHL-----NN-----SECM 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                      339 PIKGLGFVL------GAYECICKAG---FYHPGVLPVNNFRRGPDQH-- 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLVGNYSIINWHLSPEDGSIVFKEVGYYNVYAKKGERLFINEEKILWSGFSREVPFSNCS 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---ISGSTKDVSEE----AYVCLPCREG------CPFCADD-----SPCFVQED 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KYLR-----LAIISFQGLCMLLDFVSMLVVYHFRKAKSIRASGLILLETILFGSLLLYF 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EFLSWIEPFGIALILFAVLGIFLTAFVLGVFIKFRNTPIVKATNRELSYLLLFSLLCCFS 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVVILYFEPSTFRCILLRWARLLGFATVYGTVTLKLHRVLKVFLSRTAQRIPYMTGGRVM 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RMLAV-----ILLVVFWFLIGWTSSV-CQNLEKQISLI-----GQGKTSDHLIFNMCLI 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G-protein fusion receptor; CaR; calcium receptor; GluR; head injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Garrett JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     metabotropic glutamate receptor; GABABR; chimeric receptor; stroke; gamma-aminobutyric acid receptor; allosteric modulator; antagonist; spinal cord injury; epilepsy; ischaemia; hypoglycaemia; anoxia; Alzheimer's disease; hyperparathyroidism; osteoporosis; depression;
                                                                                         135 FLNVMLQSNKSREQNLQDDLDWYQALVWSLL-----EGEPSISRAAITFSTDSLSAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Busby JG,
                                                                                                                                                                                                                           239 FSELISOYSDEE-----EIQHVVEVIONSTAKV-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chimeric hCAR/hmGluR2 protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ā
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Simin RT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present amino acid sequence is an isoform of the human calcium sensing receptor CaSRd, expressed in the kidney. It is a splice variant of the wild type CaSR, that arise from deletion of amino acids 361-465, from the extracellular domain, that comprise acidic residues. It has hypotensive and osteopathic activity. The CaSR isoforms can be used to identify agonists and antagonists that modulate the receptor activity and calcium levels. These modulators are useful for treating hyperparathyroidism or osteoporosis, Paget's disease, hypercalcaemia malignancy or hypertension. The DNA sequence is also useful for altering the CaSR activity and in gene therapy.

Note: This sequence has deletion of amino acids 361-465, according to the sequence shown in the specification, but has been stated as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Calcium Sensing Receptor; CaSRd; isoform; human; splice variant; hypotensive; osteopethic; receptor activity; calcium level; modulator; treatment; hyperparathyroidism; osteoperosis; paget's disease; hypercalcaemia malignancy; hypertension; gene therapy.
                                                                                                                                   RGPD------QHISGSTKDVSEEAYVCLPCREGCPFCADDSPCFVQEDKYLRLAI 420
                                                                                                                                                                             375 RHPDGFNGTIMEIAWQEQQDNISNYYSEVFKCLPCAPGCDTCTGPEPCLANYHWPFRISL 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding isoforms of human calcium sensing receptor for treating, e.g. hyperparathyroidism or osteoporosis
  SFINKYRREHPGKLRAEVVSIWRKMSVEEKQAFQRIGTIQETPTHVHFEEEEVPVPISND 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                              --GFVLGAYECICKAGFYHPGVLPVNNFRR
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                                                                                       325 VIDIVECDYRQPSAETPTVTGGKLLTTLTGSSSWTRGSYQCLCRGGFY---
                                                                                                                                                                                                                                                    ISFQGLCMLLDFVSMLVVYHFRKAKSIRASGLILLETILFGSLLLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human calcium sensing receptor isoform, CaSRd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 24; Page 66-69; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                 AAY45000 standard; Protein; 974 AA
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Matches 114; Conservative
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                                                                                                                                                                                                                                                                                                                                                                       domain of the receptor
                                                                                                                                                                                                                                                                                                                                                      and GABABR,
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Matches 68; Conserv
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                                                                                                                                                                                                                                                                                                                               G-protein
                       WO200229033-A2
                                                                                                                                                                                                                             Stormann T,
                                                               11-APR-2002
                                                                                                                                                                                                                                                                                                                                                      mGluR
                                                                                                                                                                                                                                                   Simin RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY49127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                 Novel
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                                                                                                                                                                         The invention relates to G-protein fusion receptors (I) comprising:

(1) in the N to C direction, extracellular (ECD), transmembrane (TMD) and intracellular (ICD) domains, each chosen independently from a CaR (altracellular (ICD) domains, each chosen independently from a CaR (calcium receptor), Gluk (metabotropic glutamate receptor) and GABABR (gamma-aminobutyric acid receptor); (2) an optional linker attached to the C-terminus of ICD; and (3) a G-protein (GP) linked to ICD or the Component, are used to assess function of the various domains and to identify compounds (e.g. allosteric modulators or antagonists) that act on these domains. The modulators are potentially useful for treating or preventing diseases associated with the receptors, e.g. stroke, head or spinal cord injury, epilepsy, ischemia, hypodycaemia, anoxia, Alzheimer's disease, hyperparathyroidism, osteoporosis, cognitive disorders and depression. Nucleic acid (II) that encodes (I) is used:

(1) for recombinant production of GABABRR domains, to a binding agent, in a form more like the natural domain structure compared with use of a command of a compared with use of a contains allowed in acking one or more domains. By shuffling different domains, agents can be identified that affect particular domains of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
                                                                                                                                                                                                        (TMD) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    different
                                                           New G-protein fusion receptors and chimeras containing domains from different receptors, used to screen for modulators, potentially useful e.g. for treating or preventing stroke or Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         311 QKVDIDQCSSDGWFSGTHKC---HLNNSE-CMPIKGLGFVLGAYECICKAG---FYHPGV 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              645 ASGRELCYILLGGVFLCYCMTFIFIAKPSTAVCTLRRLGLGTAFSVCYSALLTKTNRIAR 704
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        449 ASGLILLETILFGSLLLYFPVVILYFEPSTFRCILLRWARLLGFATVYGTVTLKLHRVLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DFWSNENHTSCFELPQEYIRWGDAWAVGPVTIACLGALATL -- FVLGVFVRH-NATPVVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; G-protein fusion receptor; extracellular domain;
transmembrane domain; intracellular domain; CaR; mGluR; GABABR;
modulator identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      509 VF--LSRTAQRIPYMT-GGRVMRMLAVI----LLVVFWFLI 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :| ||| || || :: :| || || || :: IFGGAREGAQRPRFISPASQVAICLALISGOLLIVVAWLVV 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 139.5; DB 20;
; Pred. No. 0.00076;
43; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric human hCAR/hmGluR2 protein sequence.
                                                                                                                                         Disclosure; Fig 10; 255pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA015092 standard; Protein; 917 AA
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24.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68; Conservative
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WPI; 1999-610995/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 68; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   917 AA;
                   N-PSDB; AAZ31057
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receptor. Sequence

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extracellular, transmembrane and intracellular domains similar to CaR, mGluR or GABAB receptor sequences. The G-protein fusion receptors of the invention may also possess a linker joined to the carboxy terminus of the intracellular domain, and a G-protein joined to the linker. The G-protein fusion receptors of the invention are useful for identifying modulators of CaR, mGluR and GABABR for use in treating associated conditions. The present amino acid sequence was used in the production of the invention.
                                                                                                                                                                                                                fusion receptor, useful for identifying modulators of sABABR, comprises G-protein joined to the intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         311 QKVDIDQCSSDGWFSGTHKC---HLNNSE-CMPIKGLGFVLGAYECICKAG---FYHPGV 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPVNNFRRRGPDQH-----ISGSTKDVSEE----AYVCLPCREG------CPFCAD 404
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    Garrett JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASGLILLETILFGSLLLYFPVVILYFEPSTFRCILLRWARLLGFATVYGTVTLKLHRVLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention comprises G-protein fusion receptors - comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 23; Length 917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
    Busby JG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           phCaR/hmGluR2*Gqi5 fusion construct protein sequence.
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Storjohann LL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ā
                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 10; 168pp; English.
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The Invention retarders to o'protein tuston receptors (1) comprising:

Intracellular (ICD) domains, each chosen independently from a CaR (calcium receptor), diuR (metabotropic glutamate receptor) and GABABR (gamma-aminobutric acid receptor); (2) an optional linker attached to the C-terminus of ICD; and (3) a G-protein (GP) linked to ICD or the Cinker. (1), and recombinant chimeric receptors (GR) without the GP component, are used to assess function of the various domains and to identify compounds (e.g. allosteric modulators or antagonists) that act on these domains. The modulators are potentially useful for treating or preventing diseases associated with the receptors, e.g. stroke, head or spinal cord injury, epilepsy, ischemia, apposlycaemia, anoxia, Alzheimer's disease, hyperparathyroidism, osteoporosis, cognitive classion. Nucleic acid (II) that encodes (I) is used:

(1) for recombinant production of corresponding proteins; and (2) to produce cells used in screening for modulators. Use of CaR and mGluR domains allows presentation of GABABR domains, to a binding agent, in a common like the natural domain structure compared with use of incomplete receptors, lacking one or more domains. By shuffling different domains, agents can be identified that affect particular domains of a
                                                                                                                                                                                                                                                                                                                                                                                                      New G-protein fusion receptors and chimeras containing domains from different receptors, used to screen for modulators, potentially useful e.g. for treating or preventing stroke or Alzheimer's disease
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                                                                                                                                                                                                                                                                                      Garrett JE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to G-protein fusion receptors (I) comprising:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1276;
                                                                                                                                                                                                                                                                                    Busby JG,
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tive 43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Fig 12; 255pp; English.
                                                                                                                                                                                                                                                                                    Hammerland LG,
                                                                                                                                                               99WO-US07333
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nes 68; Conservative
                                                                                                                                                                                                                                            (NPSP-) NPS PHARM INC.
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N-PSDB; AAZ31058.
cognitive disorder.
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                                       Homo sapiens.
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                                                                               WO9951641-A1
                                                                                                                                                             02-APR-1999;
                                                                                                                       14-OCT-1999
                                                                                                                                                                                                                                                                                                       Simin RT
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The invention comprises G-protein fusion receptors - comprising extracellular, transmembrane and intracellular domains similar to CaR, mGluR or GABAB receptor sequences. The G-protein fusion receptors of the invention may also possess a linker joined to the carboxy terminus of the intracellular domain, and a G-protein joined to the linker. The G-protein fusion receptors of the invention are useful for identifying modulators of CaR, mGluR and GABABR for use in treating associated conditions. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present amino acid sequence was used in the production of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel G-protein fusion receptor, useful for identifying modulators of CaR, mGluR and GABABR, comprises G-protein joined to the intracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       311 QKVDIDQCSSDGWFSGTHKC---HLNNSE-CMPIKGLGFVLGAYECICKAG---FYHPGV 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Garrett JE;
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                                                                                                                                                Human; G-protein fusion receptor; extracellular domain;
transmembrane domain; intracellular domain; CaR; mGluR; GABABR;
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24.2%; Pred. No. 0.0013;
Ive 43; Mismatches 111; I
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                                                                                                            Human phCaR/hmGluR2*Gqi5 fusion construct protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Storjohann LL,
AA015093 standard; Protein; 1276 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Fig 12; 168pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43;
                                                                                                                                                                                                                                                                                                                                03-OCT-2001; 2001WO-US31074.
                                                                                                                                                                                                                                                                                                                                                                  03-OCT-2000; 2000US-0679664.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Hammerland LG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24.28;
                                                                                                                                                                                      modulator identification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 24.2 tes 68; Conservative
                                                                                                                                                                                                                      Chimeric - Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        domain of the receptor
                                                                                                                                                                                                                                                                                                                                                                                                        (NPSP-) NPS PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-330170/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1276 AA;
                                                                                                                                                                                                                                                        WO200229033-A2.
                                                                        22-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                         Stormann T,
Simin RT;
                                                                                                                                                                                                                                                                                              11-APR-2002
                                     AA015093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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2001-318282/34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DE19955408-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (FARB ) BAYER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-NOV-1999;
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244
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AAB86161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hyperparathyroidism or osteoporosis, Paget's disease, hypercalcaemia malignancy or hypertension. The DNA sequence is also useful for altering the CaSR activity and in gene therapy.

Note: This sequence has deletion of amino acids 361-537, according to the sequence shown in the specification, but has been stated as 358-536 in the claims. This sequence is not found in the specification but has been constructed from the human CaSR sequence (Seq ID.No.12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present amino acid sequence is an isoform of the human calcium sensing receptor CaSR, expressed in the kidney. It is a splice variant of the wild type CaSR, that arise from deletion of amino acids 301-537, from the extractellular domain, that comprise acidic residues. It has hypotensive and osteopathic activity. The CaSR isoforms can be used to identify agonists and antagonists that modulate the receptor activity and calcium levels. These modulators are useful for treating
                                                                                                                                                                                           Calcium Sensing Receptor; CaSR; isoform; human; splice variant; hypotensive, osteopethic; receptor activity; calcium level; modulator; treatment; hyperparathyroidism; osteopenosis; paget's disease; hypercalcaemia malignancy; hypertension; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding isoforms of human calcium sensing receptor for treating, e.g. hyperparathyroidism or osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 AEEVPMDVASYLYTGDSHQLKRANCSGRYELAGLPGKWPALASAHPSLHRALDTLTHATN 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEHIPSTIAVVGATGSGVSTAVANLLGLFYI-----POVSYASSS--RLLSNKNOFKS 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 APQVFLQATREESRILLLQDLSSSAPHLANATLETEWFHGLRRKWRPHLHRRGPNQGP--- 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                239 FSELISQYSDEE-----EIQHVVEVIQNSTAKV-----IVVFSSGPDLEPLIK 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLNVMLQSNKSREQNLQDDLDWYQALVWSLL------EGEPSISRAAITFSTDSLSAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FLRT-IPNDEHQATAMADIIEYFR---WNWVGTIAADDDYGRPGIEKFREEAEERDICID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
4.3%; Score 136; DB 21; Length 901;
Best Local Similarity 18.5%; Pred. No. 0.0016;
Matches 104; Conservative 84; Mismatches 225; Indels 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84; Mismatches
                                                                                                                                                         Human calcium sensing receptor isoform.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thrower LW;
                                               AAY45001 standard; Protein; 901 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 23; Page -; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (AVET ) AVENTIS PHARM PROD INC.
                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US17116
                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0094702.
                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Labaudiniere RF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000-195263/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 found in page 76-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   901 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAZ50617
                                                                                                                                                                                                                                                                                                                                            WO200006601-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                     28-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JUL-1998;
                                                                                                                                                                                                                                                                                         sapiens
                                                                                                                      20-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                 10-FEB-2000
                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                  AAY45001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132
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             RESULT 13
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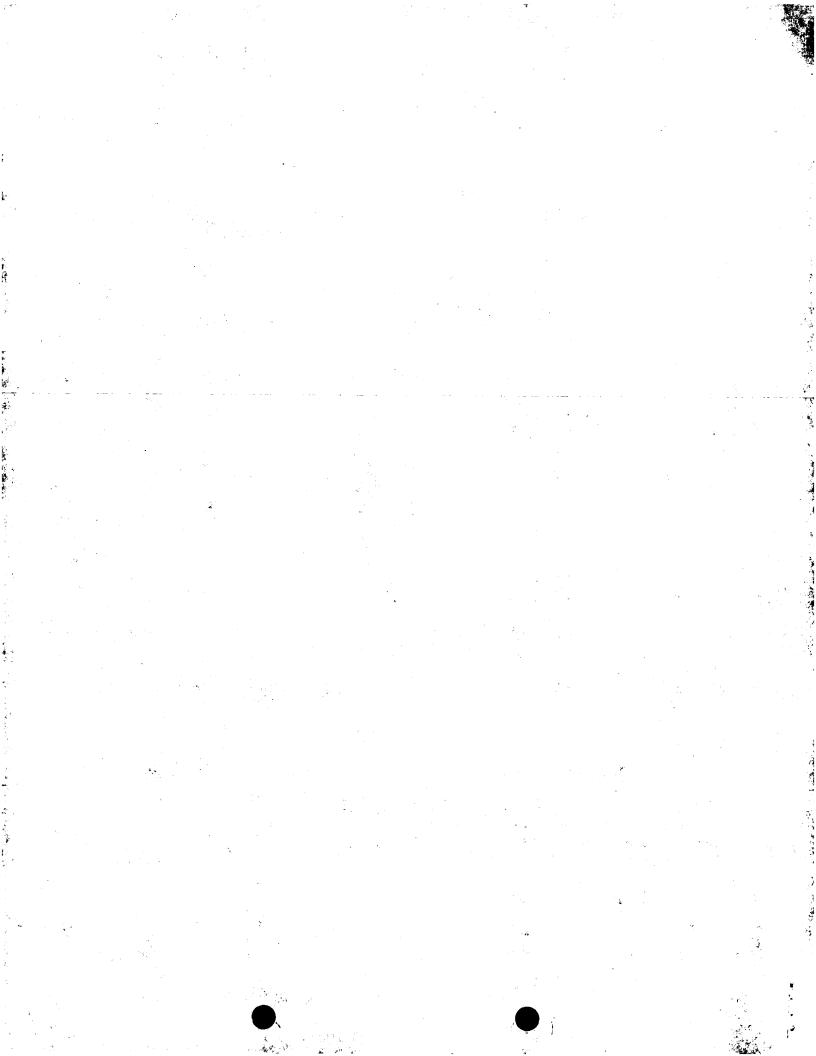
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This invention describes a novel polypeptide (I), functioning as a gamma-aminobutyric acid -B (GABA-B) receptor which has insecticidal activity. (I), also the nuclaic acid (II) that encodes it and related vectors, host cells, antibodies and transgenic invertebrates, are used for identifying: (i) new plant protection agents, i.e. modulators of (I) with insecticidal activity, which may also be useful in human or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New invertebrate gamma-aminobutyric acid receptor proteins, useful in screening for potential insecticides, for plant protection or medicine, also related nucleic acid -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       583
                                                                                                                                                        351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      504
----RGL-GHSWRRKDGLGGDKSHFKWS------PPYLECENGSYKPGWLVTLSSAIYG 291
                                                                            282 EIVRRNITGKIWLASEA------WASSSLIAMPQYFHVVGGTIG-----FA
                                                                                                                                                            LQPNLVPEFRGVMKVDINLQKVDIDQCSSDGWFSGTHKCHLNNSECMPIKGLGFVLGAYE
                                                                                                                                                                                                                                                                                                                                                                                                     -CPFCADD-----SPCFVQEDKYLR-----LAIISFQGLCMLLDFVSMLVVYHFRKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  404 ACNKCPDDFWSNENHTSCIAKEIEFLSWTEPFGIALTLFAVLGIFLTAFVLGVFIKFRNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      445 KSIRASGLILLETILFGSLLLYFPVVILYFEPSTFRCILLRWARLLGFATVYGTVTLKLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  464 PIVKATNRELSYLLLFSLLCCFSSSLFFIGEPQDWTCRLRQPAFGISFVLCISCILVKTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RVLKVFLSRTAQRIPYMTGGRVMRMLAV-----ILLVVFWFLIGWTSSV-CQNLEKQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RVLLVFEAKIPTSFHRKWWGLNLQFLLVFLCTFMQIVICVIWLYTAPPSSYRNQELEDEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GABA-B receptor; fruitfly; gamma-aminobutyric acid B receptor; insecticide; transgenic invertebrate; plant protection agent; human medicine; veterinary medicine; insect.
                                                                                                                                                                                                                                                                                                                    CICKAGFYHPGVLPVNNFRRRGPDQHISGSTKDVSEE----AYVCLPCREG-
                                                                                                                                                                                                                                    LKAGQIPGFREFLK-KVHPRKSVHNGFAKEFW-EETFNCHLPFSNC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D. melanogaster GABA-B receptor protein SEQ ID 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB86161 standard; Protein; 1305 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    557 SLI----GQGKTSDHLIFNMCLI 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                584 IFITCHEGSLMALGFLIGYTCLL 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Τ;
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SMLVVYHFRKAKSIRASGLILLETILFGSLLLYFPVVILYFEPSTFRCILLRWARLLGFA 493
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                                                                                                                                             Brown E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        434
   δλ
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                                                                                                  27;
veterinary medicine; and (11) genes that encode polypeptides involved in assembly of functionally related GABA-B receptors in insects. This sequence represents a fruitfly (Drosophila melanogaster) GABA-B receptor which is described in the method of the invention.
                                                                                                                       63 RSTDGTILAQKLAEEVPMDVASYLYTGDSHQLKRANCSGR-----YELAGLPGKWP--A 114
                                                                                                                                                                115 LASAHPSLHRALDTL----TH-----ATNFLNVMLQSNKSREQNLQDDLDWYQALVW 162
                                                                                                                                                                                                                                                                                                 314
                                                                                                                                                                                                                                                                                                                     577
                                                                                                                                                                                                                                                                                                                                           372
                                                                                                                                                                                                                                                                                                                                                                                      432
                                                                                                                                                                                                                                                                                                                                                                                                                             433 VSMLVVYHFRKAKSIRASGLILLETILFGSLLLYFPVVILYFEPST-----FRCILLR 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     344 RETDTRIIIGSFSQELAPQILCEAY-----RLRMFGADYAWILHESMGAPW-WPDQR 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WARLL--GFATVYGTVTLKLHRVLKVFLSRTAQ------RIPYMTGGRVMRMLAVI 533
                                                                                                                                                                                                          SLLEGEPSISRAAITFSTDSLSAPAPQVFLQATREESR--------ILLQDLSS
                                                                                                                                                                                                                         --FHGQDGFG-----SGYGPRISIAATQSDSRRRRRGVVGTSGGHLFPEAISQ
                                                                                                                                                                                                                                                    SAPHLANATLETEWFHGLRRKWRPHLHRRGPNQGPRGLGHSWRRKDGLGGDKSHFKWSPP
                                                                                                                                                                                                                                                                                               YLE-------CENGSYKPGWLVTLSSAIYGLQPNLVPEFRGVMKVDINLQKVD
                                                                                                                                                                                                                                                                                                            dogfish shark; SKCaR-RP; fish farming;
                                                                                                                                                                                                                                                                          491 YAPQ----TYDAVWAIALALRAAEEHWRRNEEQS------KLDGFDYTRSDMAWE--
                                                                                                                                                                                                                                                                                                                                         315 IDQCSSDGWFSGTHKCHLNNSECMPIKGLGFVLGAYECICKAGFYHPGVLPVNN--FRRR
                                                                                                                                                                                                                                                                                                                                                                                   GPDQHISGSTKDVSEEAYVCLPCREGCPFCADDSPCFVQEDKYLRLAIISFQGLCMLLDF
                                                                                                                                                                                                                                                                                                                                                                                                         -------VATIAPL-----AFYTIATLSSVGIALAITF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dogfish shark kidney calcium receptor related protein (SKCaR-RP).
                                                                           Length 1305;
                                                                                                  Indels 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note- "region in extracellular domain that is highly divergent from mammalian PVCR"
                                                                                                                                                                               | :: | :: | :: | 395 TACSNHELQLAVENLIVVSTHNSIVGNNVSYSGLNNHMFNSQLRKQSAQ----
                                                                           DB 22;
                                                                         4.2%; Score 134.5; DB 22;
18.8%; Pred. No. 0.004;
tive 80; Mismatches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Calcium receptor related protein; CaR-RP; polycation-sensing receptor; aquaculture; salinity tolerance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
351..395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLVVFWFLIGWTSSVCQNLEKQIS 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLVTLWVVTDPMERHLHNLTLEIS 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW32059 standard; Protein; 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                       Best Local Similarity 18.8 Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          870
                                                       1305 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Squalus acanthias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-MAR-1998
                                                       Sequence
                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW32059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
Region
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This protein comprises dogfish shark kidney calcium receptor related protein (SKCaR-RP), an aquatic polyvalent cation-sensing receptor (PVCR). Its amino acid sequence was deduced from a kidney cDNA clone (see ANT8990). It shows 74% homology to rat kidney cDNA clone (see ANT8990). It shows 74% homology to rat kidney prove and bowine parathyroid PVCR and possesses general features that are homologous to PVCR proteins, including a large extracellular domain. Also claimed are: an isolated PVCR present in the plasma membranes of aquatic species, especially on the apical membrane of epithelial cells of elasmobranch fish, particularly from cells found in the collecting duct or late distal tubule in the kidney, intestine, gill, rectal gland, gonad or brain; an antibody that specifically binds to a PVCR, and a method of screening for aquatic PVCR activates or inhibits aquatic PVCR mediated ion transport and endocrine changes that permit fish to adapt to fresh or salt water. The method facilitates the aquaculture of marine fish and can provide for the development of marine fish that are easily adaptable to fresh water aquaculture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                234 LHR-----RGDNQGPRGLGHSWR----RKDGL----GGDKSHFKWSPPYLECENGS 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated Aquatic polyvalent cation-sensing receptor - used to develop products for increasing or decreasing the salinity tolerance of fish for use in aquaculture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EAWQVLNHLLHLKFTNSMGEQVDFDDQGDLKGNYTINWQLSAEDESVLFHEVGNYNAYA
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Pred. No. 0.0034;
9; Mismatches 167; Indels 149;
in C-terminal domain that is divergent from mammalian PVCR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              277 YKPGWLVTLSSAIYGLQPNLVPEFRGVMKVDINLQKVDIDQCSS-----
                                                                                                                                                                                                                                                                                                                                                                                                              (BGHM ) BRIGHAM & WOMENS HOSPITAL.
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       "region
highly
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Local Similarity 19.5%; Pro
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                                                                                                                                                                                                                                                                97WO-US05031
   /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Harris HW,
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                                                                                                                                                                                                                                                            27-MAR-1997;
                                                                                                                                                                                                                                                                                                                                     27-MAR-1996;
                                                                                                                                                                                           02-OCT-1997
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----CPFCADD-----SPCFVQEDKYLR-----LAIISFQGLCMLLDFV 433

Search completed: February 15, 2003, 08:29:00 Job time : 38.7095 secs



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GenCore version 5.1.3
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- protein search, using sw model OM protein February 15, 2003, 05:55:14 ; Search time 16.1803 Seconds (without alignments) 3558.936 Million cell updates/sec Run on:

US-09-775-181-4 3199 Title: Perfect score: Sequence:

1 MGAMAYPLLLCLLLAQLGLG......XMTAVGMWSLVSYDGLTIFQ 599

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

al number of hits satisfying chosen parameters:

283224

seq length: 0 seq length: 200000000 DB DB mnmı Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote	- >	calcium receptor (	Ca(2+)-sensing rec	metabotropic gluta	calcium receptor (	metabotropic gluta							σ	MIBP1 protein - ra	ErbB kinase activa	ErbB kinase activa	delta-like homeoti	metabotropic gluta	uromodulin precurs	Tamm-Horsfall prot	thrombospondin 3 p	ptc	sodium channel SCA	matrix metalloprot	vitronectin precur	0		preadipocyte facto
SUMMARIES	ID	T27628	I59362	A56715	~	JC7160	B56715	JH0561	A41939	JC2132	JC2131	JH0562	A42916	T34513	JC5701	S53611	JC5700	JC5702	S53716	T30806	A40212	I84634	A57121	S71376	T30902	138029	JC5139	7	A55567	5478
	ength DB				1085 2																		926		993				871	
ф	Query Match Length	4.3	4.2		3.8						•		•	٠	3.4	•	•	•	•	•	•	•	•	•			٠	•	3.1	
	Score	136	133.5	127	123	120.5	119.5	116	115	114	114	112	111	110.5	109.5	107.5	106.5	106.5	106	106	104.5	104.5	104.5	100.5	100		98.2	86	86	97.5
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fibrillin 1 precur	fibrillin-2 precur	coat protein VP1 -	hypothetical prote	Motch B protein -	fibrillin-1 precur	taste receptor T1R	terminase large ch	fibrillin-2 precur	hypothetical prote	thrombospondin 3 -	opsin 2 - fruit fl	reversed polarity	metabotropic gluta	homeotic protein d
A47221 H82182	A54105	VCPVPP	G65116	A49175	A55624	JC7683	T12725	A57278	T22812	A46016	OOFF2	A54282	A49874	S53718
2 2	7	7	7	7	7	7	7	7	7	Н	-	7	~	7
3002	2918	723	986	1203	2871	828	468	2907	3871	926	381	612	915	385
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97.5	97	96.5	96.5	96.5	96.5	95.5	95	95	95	94.5	94	94	94	93.5
30	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

RESULT 1 T27628 hypothetical protein ZC506.4 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: L3-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000 C;Accession: T27628 R;Harris, B.	submitted to the EMBL Data Library, December 1994 A;Reference number: 220395 A;Accession: T27628 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA	A;Residues: 1-999 <wil> A;Cross-references: EMBL:247073; PIDN:CAA87374.1; GSPDB:GN00028; CESP:2C506.4 A;Experimental source: clone 2C506</wil>	Cycenetics: A;Gene: CESP:2C506.4 A;Map position: X A;Introns: 32/2; 65/3; 77/3; 113/2; 140/3; 177/2; 240/2; 277/1; 315/2; 439/2; 471/3; C;Superfamily: metabotropic glutamate receptor 4	Query Match 4.3%; Score 136; DB 2; Length 999; Best Local Similarity 22.3%; Pred. No. 0.035; Matches 48; Conservative 44; Mismatches 87; Indels 36; Gaps 8;	354 CKAGFYHPGVLPVNNFRRGPDQHISGSTKDVSEEAVVCLPCREGCPFCADDSPC 408		)	2y 458 ILFGSLLLYFPVVILYFEPSTFRCILLRWARLLGFATVYGTVTLKLHRVLKVFLSRTAGR 517		2y 518IPYMIGGRVMRMLAVILLVVFWFLIGW 544	
RES T27 Dyy C;S C;I	Sul A; E A; E A; E	A A ;	O A A A C	<u>ош 2</u>	Qy Db	QY	qq	QY	qq	QY	QΩ

# RESULT 2 I59362

calcium/polyvalent cation-sensing receptor precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Species: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999
C:Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 05-Nov-1999
C:Accession: I59362; A55594
R:Ruat, M.; Molliver, M.E.; Snowman, A.M.; Snyder, S.H.
Proc. Natl. Acad sci. U.S.A. 92, 3161-3165, 1995
A;Title: Calcium sensing receptor: anolecular cloning in rat and localization to nerve
A;Reference number: I59362; MUID:95241465; PMID:7724534

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gene cause familial hypocalci
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A;Note: sequence modified after extraction from NCBI backbone
A;Note: 186-Arg mutation is associated with familial hypocalciuric hypercalcemia and
A;Note: sequence extracted from NCBI backbone (NCBIN:142453)
A;Accession: B49419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Note: 298-Lys mutation is associated with familial hypocalciuric hypercalcemia and A;Note: sequence extracted from NCBI backbone (NCBIN:142455)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypercalcemia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A)Residues: 1-180.70,,182-989,78',991-1078 <PEA>
A)Cross-references: EMBL:X81086

R)Forblak, M.R.; Brown, E.M.; Chou, Y.H.; Hebert, S.C.; Marx, S.J.; Steinmann, B.; ]
Cell 75, 1297-1303, 1993

A)Title: Mutations in the human Ca(2+)-sensing receptor gene cause familial hypocanay, A; Reference number: A49419; MUID:94094324; PMID:7916660
                                                    parathyroid calcium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               405 D-----SPCFVQEDKYLR-----LAIISFQGLCMLLDFVSMLVVYHFRKAKSIRASG 451
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                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-1078 <GAR>
A; Cross-references: GB: UZ0759; NID: g683744; PIDN: AAA86503.1; PID: g683745
R; Pearce, S.H.S.; Thakker, R.V.
Submitted to the EMBL Data Library, August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          475 EQVTFDEC---GDLVGNYSIINWHLSPEDGSIVFKEVGY----YNVYAKKGERLFINEEK
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A; Note: sequence modified after extraction from NCBI backbone
A; Note: 796-Trp mutation is associated with familial hypocalciuric
A; Note: sequence extracted from NCBI backbone (NCBIN:142457)
C; Keywords: 91ycoprotein; receptor; transmembrane protein
                                                        human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A) Experimental source: family E
A) Note: sequence modified after extraction from NCBI backbone
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             J. Biol. Chem. 270, 12919-12925, 1995
A;Title: Molecular cloning and functional expression of
A;Reference number: A56715; MUID:95279439; PMID:7759551
A;Accession: A56715
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22.5%; Pred. No. C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 178-192 <POL>
A;Experimental source: family N
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A; Accession: S49341
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A; Residues: 289-303 <PO2>
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A; Residues: 788-802 <P03>
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A:Experimental source: Kidney

A:Experimental source: Kidney

F.1-20/Domain: signal sequence #status predicted <SIG>
F.187-212/Region: hydrophobic

B:187-212/Region: hydrophobic

B:187-212/Region: hydrophobic

B:187-212/Region: hydrophobic

B:187-212/Region: hydrophobic

B:187-212/Region: hydrophobic

B:187-212/Region: transmembrane #status predicted <TMA>

B:187-212/Region: transmembrane #status predicted <TMA>

F:725-744/Domain: transmembrane #status predicted <TMA>

F:707-790/Domain: transmembrane #status predicted <TMA>

F:708-790/Domain: transmembrane #status predicted <TMA>

F:709-790/Domain: transmembrane #status predicted <TMA>

F:708-790/Domain: transmembrane #status predicted <TMA>

F:709-790/Domain: transmembrane #status predicted <TMA

F:707-790/Domain: transmembrane #status predicted <TMA

F:708-790/Domain: transmembrane #status predicted <TMA

F:709
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C;Species: Homo sapiens (man)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 01-Dec-2000
C;Accession: A56715; 849341; A49419; B49419; C49419
R;Garrett, J.E.; Capuano, I.V.; Hammerland, L.G.; Hung, B.C.P.; Brown, E.M.; Hebert, S.
18;
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C;Date: 19-Oct-1995 #text_change 21-Jul-2000
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 21-Jul-2000
C;Accession: B56715
R;Garrett, J.E.; Capuano, I.V.; Hammerland, L.G.; Hung, B.C.P.; Brown, E.M.; Hebert, J. B.; Capuano, I.V.; Hammerland, L.G.; Hung, B.C.P.; Brown, E.M.; Hebert, A; Eitle: MOlecular cloning and functional expression of human parathyroid calcium revA;Reference number: A56715; MUID:95279439; PMID:7759551
                                                                                                                                                                                                                                                                         138 VMLQSNKSRE----QNLQDDLDWYQALVW----SLLEGEPSISRAAITFSTDSLSAPAP 188
                                                                                                                                                                                                                                                                                                                                                                                                                           189 QVFLQATREESRILLQDLSSSAPHLANATLETEWFHGLRRKWRPHLHRRGPNQGPRGLGH 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    515 PNEMKNMQPGDVCCWICIPCEPYEYLVDEFTCMDCGPGQWPTADLSGCYNLPEDYIRWED 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      343 LGFVLGAYECICKAGFYHPGVLPVNNFRRRGPDQHISGSTKDVSEE----AYVCLPCREG 398
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A.Molecule type: mRNA
A.Residues: 1-1088 <GAR>
A.Residues: 1-1088 <GAR>
A.Cross-references: GB:U20760; NID:g683746; PIDN:AAA86504.1; PID:g683747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YGDGMGRYNVFN----FQHIGGKYSYLKVGHWAETLYLDVDSIHWSRNSVPTSQCSDPCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----AVVCLPCRE-----GCPFC-----ADDSPCFVQEDKYLR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----LAIISFQGLCMLLDFVSMLVVYHFRKAKSIRASGLILLETILFGSLLLYFPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  470 VILYFEPSTFRCILLRWARLLGFATVYGTVTLKLHRVLKVF--LSRTAQRIPYMT-GGRV
                                                                                                                                                                                              Indels 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1088,
                                                                                                                                                                                                                                                                                                                        Length
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           #status predicted <TM6>
#status predicted <TM7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117;
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Pred. No. 0.73;
38; Mismatches
                                                                                                                  Score 120.5; Di
Pred. No. 0.46;
                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      calcium receptor (clone phPCaR-5.2) - human
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                                                                                                                      3.8%;
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F;770-791/Domain: transmembrane F;804-828/Domain: transmembrane
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Best Local Similarity 22.89
                                                                                                                                                                                                 Conservative
                                                                                                                                                      Local Similarity
les 91; Conserv
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                                                                                                                  Query Match
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R;Minoshima, T.; Nakanishi, S.
J Blochem. 1271,80 899 896, 1999

A;Title: Structural organization of the mouse metabotropic glutamate receptor subtype 3

A;Title: Structural organization of the mouse metabotropic glutamate receptor subtype 3

A;Reference number: JC7160; MUID:20012997; PMID:10544282

A;Reference number: JC7160; MUID:20012997; PMID:10544282

A;Residues: 1-879 AINA

A;Residues: 1-879 AINA

A;Residues: 1-879 AINA

A;Coss-references: GB:AF170696

C;Genetics: A;Gene: mGlun3

C;Superfamily: metabotropic glutamate receptor 4

C;Keywords: differentiation; G protein-coupled receptor; transmembrane protein

F;1-24/Domain: signal sequence #status predicted <TM1>
F;517-599/Domain: transmembrane #status predicted <TM2>
F;644-664/Domain: transmembrane #status predicted <TM3>
F;644-664/Domain: transmembrane #status predicted <TM3>
F;689-709/Domain: transmembrane #status predicted <TM3>
F;735-756/Domain: transmembrane #status predicted <T
                                                                                                                                                                              Ca(2+)-sensing receptor - bovine
CiSpecies: Bos primigenius taurus (cattle)
CiSpecies: Bos primigenius taurus (cattle)
CiSpecies: Bos primigenius taurus (cattle)
CiSpecies: Bos primigenius taurus (sequence_revision 19-Mar-1997 #text_change 05-Nov-1999
CiSpacession: S40476
Ribrown, E.M.; Gamba, G.; Riccardi, D.; Lombardi, M.; Butters, R.; Kifor, O.; Sun, A.; Nature 366, 575-580, 1993
Nature 366, 575-580, 1993
A;Title: Cloning and characterization of an extracellular Ca(2+)-sensing receptor from A;Reference number: S40476; MUID:94077182; PMID:8255296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
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Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311 QKVDIDQCSSDGWFSGTHKC---HLNNSE-CMPIKGLGFVLGAYECICKAG---FYHPGV 363
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A;Moleoule type: mRNA
A;Residues: 1-1085 <BRO>
A;Cross-references: GB:S67307; NID:g453108; PIDN:AAB29171.1; PID:g453109
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Pred. No. 0.39;
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21.1%;
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GSLMALGFLIGYTCLL 783
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417

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Gaps

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Grotein-coupled glutamate receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Accession: A41939; 815362
R;Houamed, K.M.; Kuijper, J.L.; Gilbert, T.L.; Haldeman, B.A.; O'Hara, P.J.; Mulvihil
S;Glence 252, 1318-1321, 1991
A;Title: Cloning, expression, and gene structure of a G protein-coupled glutamate rec
A;Reference number: A41939; MUD:92022526; PMID:1656524
A;Accession: A41939
A;Status: pre-liminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-1199 <HGOT9
A;Residues: 1-1199 <HGOT9
A;Residues: 1-1199 <HGOT9
A;Residues: 1-1199 <HGOT9
A;Cross-references: GB:M61099; NID:9397806; PIDN:AA419497.1; PID:g204460
A;Experimental source: cerebellum
A;Mote: sequence extracted from NCBI backbone (NCBIP:60785)
A;Masu, M.; Tanabe, Y.; Tsuchida, K.; Shigemoto, R.; Nakanishi, S.
Nature 349, 760-765, 1991
A;Title: Sequence and expression of a metabotropic glutamate receptor.
A;Reference number: S15362; MUDD:91156047; PMID:18479955
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C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Jan-1996
C;Accession: JC2132
R;Minakami, R.; Katsuki, F.; Yamamoto, T.; Nakamura, K.; Sugiyama, H.
Biochan. Biophys. Res. Commun. 199, 1136-1143, 1994
A;Title: Molecular cloning and the functional expression of two isoforms of human
   572 VTIACLGALATL--FVLGVFVRH-NATPVVKASGRELCYILLGGVFLCYCMTFVFIAKPS 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   615 VLYRDTPVVKSSSRELCYIILAGIFLGYVCPFTLIAKPTTTSCYLQRLLVGLSSAMCYSA 674
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                                                                                                             478 TFRCILLRWARLLGFATVYGTVTLKLHRVLKVF--LSRTAQRIPYMT-GGRVMRMLAVI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            675 LVTKTNRIARILAGSKKKICTRKPRFMSAWAQVIIASILISVQLTLVVTLII-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108; Indels
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1.8;
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Pred. No. 1
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Best Local Similarity 20.7%;
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                                                                                                                                                                                                                                                        |:| | ::
689 GQLLIVAAWLVV 700
                                                                                                                                                                                                                ---LLVVFWFLI 542
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A; Residues: 1-1199 <MAS>
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A. Residues: 1-872 cTAN.
A. Residues: 1-872 cTAN.
A. Residues: 1-872 cTAN.
A. Experimental Source: brain
C. Comment: This protein is coupled to a G protein and evokes a variety of functions by m C. Superfamily: metabotropic glutamate receptor 4
C. Superfamily: metabotropic glutamate receptor 4
C. Superfamily: metabotropic glutamate receptor 2
F. 19-872/Product: metabotropic glutamate receptor 2 #status predicted cXIG.
F. 19-872/Product: metabotropic glutamate receptor 2 #status predicted cXIG.
F. 56-590/Domain: transmembrane #status predicted cXII.>
F. 665-625/Domain: transmembrane #status predicted cXII.>
F. 637-655/Domain: transmembrane #status predicted cXII.>
F. 637-655/Domain: transmembrane #status predicted cXIV.>
F. 76-747/Domain: transmembrane #status predicted cXIV.>
F. 76-782/Domain: transmembrane #status predicted cXIV.>
F. 76-819/Domain: transmembrane #status predicted cXIV.>
F. 76-819/Domain: transmembrane #status predicted cXIV.>
F. 76-782/Domain: transmembrane #stat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species: Rattus norvegicus (Norway rat)
Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Sep-1998
Eccession: JH0561
LVVYHFRKAKSIRASGLILLETILFGSLLLYFPVVILYFEPSTFRCILLRWARLLGFATV 495
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                                                                                                                                                                                   : :| :|| || || :: | | | :: | | | :: | | | ISCILVKTNRVLLVFEAKIPTSFHRKWWGLNLQFLLVFLCTFMQIVICVIWLYTAPPSSY 761
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                                                                                                                                       YGTVTLKLHRVLKVFLSRTAQRIPYMTGGRVMRMLAV-----ILLVVFWFLIGWTSSV
                                                                 GVFIKFRNTPIVKATNRELSYLLLFSLLCCFSSSLFFIGEPODWTCRLROPAFGISFVLC
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18.9%; Pred. No. 1;
tive 63; Mismatches 184; Indels 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                danabe, Y.; Masu, M.; Ishii, T.; Shigemoto, R.; Nakanishi, S.
Suron 8, 169-179, 1992
Tritle: A family of metabotropic glutamate receptors.
Reference number: JH0561; MUID:921100002; PMID:1309649
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Best Local Similarity 18.95
Matches 93; Conservative
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436
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A; Molecule type: mRNA
A; Residues: 1-879 <TAN>
A; Experimental source: brain
C; Comment: This protein is coupled to a G protein and evokes a variety of functions b C; Superfamily: metabotropic glutamate receptor 4
C; Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane predicted <SIG>
E; 23-879/Product: metabotropic glutamate receptor 3 #status predicted <MET>
F; 517-599/Domain: transmembrane #status predicted <TRI>
F; 644-664/Domain: transmembrane #status predicted <III>
F; 645-650/Domain: transmembrane #status predicted <III>
F; 689-709/Domain: transmembrane #status predicted <IIV>
F; 804-828/Domain: transmembrane #status predicted <IIV>
F; 804-828/Domain: transmembrane #status predicted <III>
F; 804-828/Domain: transmembrane #status predicted <IIII>
F; 804-828/Domain: transmembrane #status predicted <IVIII>
F; 804-828/Domain: transmembrane #status predicted <IVIII->
F; 805-829-82414, 439/Binding site: phosphate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 13-Sep-1998
C;Accession: JH0562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRWARLLGFATVYGTVTLKLHRVLKVF--LSRTAQRIPYMT-GGRVMRMLAVIL----LV 536
                                                                        ::|| | | | | : | | | | DVKWEDDYYLKLRPETHHRNP-----WFQEFWQHRFQCRLEGFPQENSKYNKT-----CN 382
                                                                                                                                                 NG-----SYKPGWLV-TLSSAIYGL---OPNLVPEFRGV------MKVDINLO 311
                                                                                                                                                                                  SSLTLKTHHVQDSKMGFVINAIYSMAYGLHNMQMSLCPGYAGLCDAMKPIDGRKLLESLM 442
                                                                                                                                                                                                                                                           KVDIDQCSSDGWFSGTHKCHLNNSECMPIKGLGFVLGAYECICKAGFYHPGVLPVNNFRR 371
                                                                                                                                                                                                                                                                                         -----ADD-SPCFVQEDKYLR-----LAIISFQGLCMLLDFVSMLVVYHFRKAKSIRA 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              553 QLGSWPTDDLTGCDLIPVQYLRWGDPEPIAAVVFACLGLLATLFVTVVFIIYRDTPVVKS 612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGLILLETILFGSLLLYFPVVILYFEPSTFRCILLRWARLLGFATVYGTVTLKLHRVLKV 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----LAIISF 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               529 WICIPCEPYEYLVDEFTCMDCGPGQWPTADLSGCYNLPEDYIKWEDAWAIGPVTIACLGF 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 424 QGLCMLLDFVSMLVVYHFRKAKSIRASGLILLETILFGSLLLYFPVVILYFEPSTFRCIL 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --RKDGLGGDKSHFKWSPPYLECE 273
                                                                                                                                                                                                                                                                                                                                                                  RGPDQHI----SGSTKDVSEE-----CPFC
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Neuron 8, 169-179, 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                metabotropic glutamate receptor 3 precursor - rat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           510 FLSRTAQRI----PYMTGGRVMRMLAVILLVV 537
                                         ETEWFHGLRRKWRPHLHRRGPNQGPRGLGHSWR-
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A;Reference number: JC2131; MUID:94197696; PMID:7908515
A,Accession: JC2132
A;Molecule type: mRNA
A;Residues: 1-1180 <MIN>
C;Comment: This protein is coupled to guanine nucleotide binding proteins.
C;Comment: This protein is coupled to guanine nucleotide binding proteins.
C;Comment: This protein is coupled to guanine predicted cyml>
F;580-604/Domain: transmembrane #status predicted cyml>
F;617-637/Domain: transmembrane #status predicted cyml>
F;647-664/Domain: transmembrane #status predicted cyml>
F;788-759/Domain: transmembrane #status predicted cyml>
F;788-759/Domain: transmembrane #status predicted cyml>
F;78-779/Domain: transmembrane #status predicted cyml>
F;78-779/Domain: transmembrane #status predicted cyml>
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ite: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 05-Jan-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSLTLKTHHVQDSKMGFVINAIYSMAYGLHNMQMSLCPGYAGLCDAMKPIDGRKLLESLM 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        493 KMDDDEVWSKKSNIIRSVCSEPCEKGQIKVIRKGEVSCCWTCTPCKENEYVFDEYTCKAC 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSRELCYIILAGICLGYLCTFCLIAKPKQIYCYLQRIGIGLSPAMSYSALVTKTNRIARI 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             219 ETEWFHGLRRKWRPHLHRRGPNQGPRGLGHSWR-----RKDGLGGDKSHFKWSPPYLECE 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   443 KTNFTGVSGDTILFDENGDSPGRYEIMNFKEMG------KDYFDYINVGSWDNGEL 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                             94;
                                                                                                                                                                                                                                                                                                                                                                                        3.6%; Score 114; DB 2; Length 1180; 20.4%; Pred. No. 2.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           53; Mismatches 165; Indels
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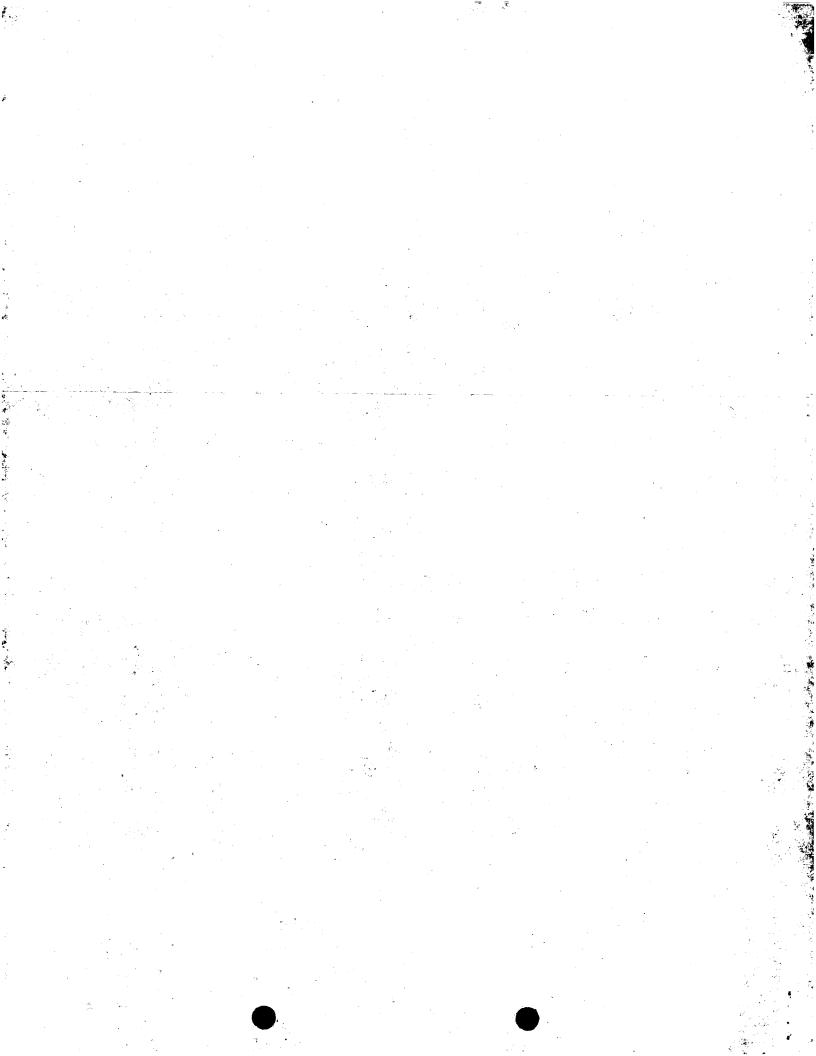
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Conservative
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A; Residues: 128-162 <HI2>
                                                                                                                                                                   Best Local Similarity
Matches 76; Conserv
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les 92; Conserv
                                                      A; Gene: CESP: ZK783.1
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metabotropic glutamate receptor mGluR5 - rat
metabotropic glutamate receptor mGluR5 - rat
c;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C;Datesion: A42916
R;Abe, T.; Sugihara, H.; Nawa, H.; Shigemoto, R.; Mizuno, N.; Nakanishi, S.
J. Biol. Chem. 267, 13361-13368, 1992
A;Title: Molecular characterization of a novel metabotropic glutamate receptor mGluR5 of A;Reference number: A42916; MUID: 92317054; PMID: 1320017
                                                                                                                                                                                                                                                                                                                                                       A;Residues: 1-1171 <ABE>
A;Residues: 1-1171 <ABE>
A;Cross-references: GB:D10891; NID:g220813; PIDN:BAA01711.1; PID:d1002186; PID:g220814
A;Experimental source: brain
A;Experimental source: brain
A;Note: sequence extracted from NCBI backbone (NCBIN:107749, NCBIP:107750)
C;Keywords: G protein-coupled receptor; transmembrane protein
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T34513
T34513
T34513
C; Datcical protein ZK783.1 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C; Accession: T34513
A; Favello, A: Vaudin, M.
Submitted to the EMBL Data Library, August 1994
A; Reference number: Z1536
A; Reference number: Z1536
A; Reference number: Z1536
A; Reference number: L1536
A; Reference number: L1536
A; Reference number: L1536
A; Reference number: L1536
A; Residues: L1537 < FAV>
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RRLGLGTSFAICYSALLTKTNCIARIFDGVKNGAQRPKFISPSSQVFICLGLILVQIVMV 703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          || : | : :|| : ::| | CDLTGCDLIPVQYLRWGDPEPIAAVVFACLGLLATLFVTVIFIIYRDTPVVKSSSRELCY
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$; Pred. No. 3.6;
54; Mismatches 171; Indels
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Best Local Similarity 20.8%
Matches 80; Conservative
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                                     537 VFWFLI 542
                                                            SVWLIL 709
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C;Accession: JC5701; PC4411
R;Higashiyama, S.; Horikawa, M.; Yamada, K.; Ichino, N.; Nakano, N.; Nakagawa, T.; Ml
J. Blochem. 122, 675-680, 1997
A;Title: A novel brain-derived member of the epidermal growth factor family that inte
A;Reference number: JC5700; MUID:98006324; PMID:9348101
                                                                                                                                                       A;Map position: 3
A;Introns: 14/1; 48/2; 84/1; 196/3; 303/1; 381/1; 586/1; 605/1; 1175/3; 1207/1; 1409/
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A;Cross-references: EMBL:U13646; PIDN:AAC24418.1; GSPDB:GN00021; CESP:ZK783.1
A;Experimental source: strain Bristol N2; clone ZK783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-868 <HTG>
A;Cross-treferences: DDBJ:D89995; NID:g2605629; PIDN:BAA23344.1; PID:g2605630
A;Accession: PC4411
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C;Date: 25-Nov-1997 #sequence_revision 25-Nov-1997 #text_change 02-Aug-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1227 GDNGETSGVDGKPTTPAPTPSSSAESSTSRIPTTSEASPEGGSGEAGVPESPDGSGESST 1286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1323 TSKPTAEP-----LETTAPSTEVTSP--EGSGTEESTLPPT----EGSGESTTSSAPTVE 1371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----RKADD----GSCODIDE----CTEHNSTC--CGANAKCVNKP 1514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SASDSSAPWSRSTDGTILAQKLAEEVPMDVASYLYTGDSHQLKRANCSGRYELAGLPGKW 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 HLHRRGPNQGPRGLGHSWRRKDGLGGDKSHFKWSPPYLECENGSYKPGWLVTLSSAIYGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             293 QPNLVPEFRGVMKVDINLQKVDIDQCSSDGWFSGTHKCHLNNSECMPIKGLGFVLGAYEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RAAITFSTDSLSAPAPQVFLQATREESRILLQDLSSSAPHLANATLETEWFHGLRRKWRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1372 PATVLPPQNRNEKPEP-----TKDTFALPTTTGAPQANDSSVE------
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C;Superfamily: human ErbB Kinase activator alpha, brain and thymus; F;361-397/Domain: EGF homology <EGF>
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18.0%; Pred. No. 16;
iive 51; Mismatches 137;
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Search completed: February 15, 2003, 08:32:14 Job time: 27.1803 secs
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A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: U; 132.263, K',2265-2437 <RON>
A;Cross-references: GB:M65251; NID:9202790; PIDN:AAA40698.1; PID:9202791
B;Mitchelmore, C.; Traboni, C.; Cortese, R.
Nucleic Acids Res. 19, 141-147, 1991
A;Title: Isolation of two cDNAs encoding zinc finger proteins which bind to the alpha 1-A;Reference number: I58280; MUID:91187610; PMID:1901405
A;Accession: S22292
A;Status: nucleic acid sequence not shown
A;Residues: 'E',1729, 'R', 1734-2437 <MIT>
A;Residues: 'E',1729, 'R', 1734-2437 <MIT>
A;Cross-references: EMBL:X54249; NID:957517; PIDN:CAA38150.1; PID:957518
A;Note: the authors did not translate the codon for residue 1
C;Superfamily: HIV-EP2 enhancer-binding protein
C;Reywords: DNA binding; duplication; metal binding; transcription regulation; zinc fing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Naticernate names: angiotensinogen gene-inducible enhancer-binding protein; c-myc intron C; Species: Rattus norvegicus (Norway rat)
C; Date: 15-Jul-1995 #sequence_travision 01-Sep-1995 #text_change 20-Jun-2000
C; Accession: 853611; A39796; S22292; IS8280
R; Makino, R.; Akiyama, K.; Yasuda, J.; Mashiyama, S.; Honda, S.; Sekiya, T.; Hayashi, K. Mucleic Acids Res. 22, 8579-5685, 1994
A; Title: Cloning and characterization of a c-myc intron binding protein (MIBP1).
A; Reference number: S53611; MUID:95140632; PMID:7838722
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A; Cross-references: EMBL:D37951; NID:g1408559; PIDN:BAA07168.1; PID:g662296
R; Ron, D.; Brasier, A.R.; Habener, J.F.
R; Ron, D.; Brasier, B.R.; Habener, J.F.
A; Title: Biol. 11, 2887-2895, 1991
A; Title: Angiotensinogen gene-inducible enhancer-binding protein 1, a member of a new A; Reference number: A39796; MUID:91203912; PMID:2017183
---QKLAEEVPMDVASYLY-----TGDSHQLKRANCSGRYELAGLPGKWPALASAHPSL 122
                                                                                                                                                                                           123 HRALDTLTHATNFLNVMLQSNKSREQNLQ----DDLDWYQALVWSLLEGEPSISRAAITF 178
                                                                                                                                                                                                                                                                                                                                                                  ----- RPKLKKMK 259
                                                                                                                                                                                                                                                                                                                                                                                                                            291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STDSLSAPPAQVFLQATREESRILLQDLSSSAPHLANATLETEWFHGLRRKWRPHLHRRG
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                                                                                                                                134 KSVQDQAYKAPVVVEGKVQGLAPAGGSSSNSTREPPASGRVALVKVLDKWP
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S53611
MIBPl protein - rat
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1337 VP-SYGSVMYTSISQILGQNS------PAIV----ICKVDENMTQRTLVTN 1376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1278 GASGLHSKNLPPKFPSDPGSKSTEAPPTEQLLREDFASENAGP-LQSLPGTVVPVRIQTH 1336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 VPMDVASYLYTGDSHQLKRANCSGRYELAGLPGKWPALASAHPSLHRALDTLTHATNFLN 137
                                                                                                                                                                                                                                                                                                                                                                                                                       18 GLGAVGASRDPQGRPDSPRERTPKGKPHAQQPGRASASDSSAPWSRSTDGTILAQKLAEE 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1435 RMLSPASSLELFMETKQQKRVKEEKMYGQIVEEL--SAVELINSDIK----KGLSRPQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VMLQS---NKSREQNLQDDLDWYQALVWSLLEGEP-----SISRAAITFST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HLHRRGPNQGPRGLGHSWRRKDGL-----GGDKSHFKWS---PPYLECENGSYKPGWLVT
                                                                                                                                                                                                                                                                                         Length 2437;
                                                                                                                                                                                                                                                                                     3.4%; Score 107.5; DB 2; Illarity 21.1%; Pred. No. 17; Conservative 54; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         285 LSSAIYGLQPNLVPEFRGVMKVDINLQKVDIDQCSSD 321
                                                                                                                                                                                                                                                                                  Score 107.5;
Pred. No. 17;
F;191-211/Region: zinc finger CCHH motif F;219-241/Region: zinc finger CCHH motif F;934-940/Region: nuclear location signal F;947-979/Region: serine-rich F;1792-1812/Region: zinc finger CCHH motif F;1820-1842/Region: zinc finger CCHH motif F;1890-1917/Region: acidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DSLSAPAPQVFLQATREESRI - - -
                                                                                                                                                                                                                                                                                                                      Best_Local Similarity
Matches 71; Conserv
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

February 15, 2003, 04:22:33 ; Search time 9.24587 Seconds (without alignments) 2687.074 Million cell updates/sec Run on:

US-09-775-181-4 3199 1 MGAMAYPLLLCLLLAQLGLG......xMTAVGMWSLVSYDGLTIFQ 599 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 segs, 41476328 residues Searched:

112892 Patal number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries imum DB seq length: 0
Maximum DB seq length: 200000000

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

IES	escription			96\db60	P48442	P41180	P35384 bos t			Q13255 homo		P23385 rattu	P41594	P31422	P31424 rattus norv			P80370 homo	P27590 rattu		Q9nyq7 homo	Q9y345 homo	Q14833 homo	O88278 rattu	09v595			P488	P981	P229	P35555 homo	Q14831 homo	095486 hошо	DOCE PORCE
SUMMARIES	ID	MGR_DROME	MGR1_CAEEL	CASR_MOUSE	CASR_RAT	CASR_HUMAN	CASR_BOVIN	MGR2_HUMAN	MGR2_RAT	MGR1_HUMAN	MGR3_HUMAN	MGR1_RAT	MGR5_HUMAN	MGR3_RAT	MGR5_RAT	NRG2_RAT	NRG2_HUMAN	DLK_HUMAN	UROM_RAT	TSP3_HUMAN	CLR3_HUMAN	S6A5_HUMAN	MGR4_HUMAN	CLR3_RAT	DCUP_DROME	NTC2_HUMAN	MM15_HUMAN	VTNC_PIG	FBN1_BOVIN	COA2_PAVPN	FBN1_HUMAN	MGR7_HUMAN	S24A_HUMAN	FRN2 HIMAN
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æ	Query Match	5.	•	٠	4.2		3.8	•	•	٠			•	3.5	•		٠	•	•	•		3.5	•	•	٠		•	•	٠	•	3.0	3.0	3.0	~
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YHDP_ECOLI NTC2_MOUSE FBN1_MOUSE FBN2_MOUSE FBN2_MOUSE TSP3_MOUSE OFS2_DROME MGR7_RAT NID2_MOUSE DLK_MOUSE DLK_MOUSE	
986 2470 2871 2871 2907 956 381 915 1403 385 621 808	
QQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQ	
48888888888888888888888888888888888888	

## ALIGNMENTS

Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., I Palazzolo M., Pittman G.S., Pan S., Pollard J., Pur: Reinert K., Remington K., Saunders R.D.C., Scheeler
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01-NOV-1997
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Q09630;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Zheng X.H., Zhong F.N., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O. Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., "The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SREQNLQDDLDWYQALVW----SLLEGEPSISRAAITFSTDS-LSAPAPQVFLQATREES 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R-----ILLQDLSSSAPHLANATLETEWFHGLRRKWRPHLHRRGPNQGPRG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                  -:- SUBCELLULAR LOCATION: Integral membrane protein.
-:- DEVELOPMENTAL STAGE: EXPRESSED IN THE CNS OF THE LATE EMBRYO.
-:- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane; Glycoprotein; Signal.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 976;
                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL METABOTROPIC GLUTAMATE RECEPTOR
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V (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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TOPLASMIC (POTENTIAL).
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10.1%; Pred. No. 0.00013;
ve 80; Mismatches 179;
                                                                                                                                                                                                                                                                            EMBL; AE003846; AAF59402.1; -
FlyBase; FB900019985; Glu-RA.
InterPro; IPR001828; MNE_receptor.
InterPro; IPR000337; GPCR_MGr.
Pfam; PF00003; 7tm_3; 1.
Pfam; PF00004; ANE_receptor; 1.
PROSITE; PS0094; GPCRMCR.
PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
G_PROTEIN_RECEP_F3_3; 1.
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                                                                                                       ! - FUNCTION: RECEPTOR FOR GLUTAMATE.
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--LECENG 275
                                                                                                                   CDDSYRLSEKVGYEQESKTQFVVDAVYAFAYALHNLHNDRCNTQSDQTTETRKHLQSESV 459
                                                                                                                                                                                                                                             ---IYGLOPNLVPEFRGVMKVDI-NL 310
                                                                                                                                                                                                                                                                                                                                                                 WYRKISTDTKSQACPDMANYDGKEFYNNYLLNVSFIDLAGSEVKFDRQGDGLARYDILNY 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QKVDIDQCSSDG------WFSGTHKCHLNNSECMPIKGLGFVLGAYECICKAGFYHPG 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----IKKQQGDTCCWICDSCESFEYVYDEFTCKDCGPGLWPYADKLSCYALDIQYMKW 622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  467 FPVVILYFEPSTFRCILLRWARLLGFATVYGTVTLKLHRVLKVF--LSRTAQRIPYMTGG 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               677 CNTFALIAKPIIGSCVLQRFGIGVGFSIIYSALLTKINRISRIFHSASKSAQRLKYISPQ 736
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-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
-!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
STRONGEST, TO MGLUR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QR----QENSSGYQYKVIGKWFNG---LQLNSETVVWNKETEQPTSACSLPCEVGM----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                363 VLPVNNFRRRGPDQHI----SGSTKDVSEEAYVCLPCREGCPFCADDSPCFVQEDKYLR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01.NOV-1997 (Rel. 35, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Probable metabotropic glutamate receptor mgl-1.
MGL-1 OR ZC506.4.
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LGHSWRRKDGLGGD - - - KSHFKWSPPY -
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SEQUENCE FROM N.A.
STRAIN=Bristol N2;
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                                                                                                                                                                                                                                                                    517
                                                                                                                                                                                                                                                                                CASR_MOUSE STANDARD; PRT; 1079 AA.
090296; 008968; 088519; 090295; 090208; 09R1D6; 09R1Y2;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Extracellular calcium-sensing receptor precursor (CaSR) (Parathyroid Cell calcium-sensing receptor).
ANS OR GPRC2A.
                                                                                                                                                                                                 615 CKIGFR-----KQLIKDEQCCWACSKCEDYEYLINETHCVGCEOGWWPTKDRKGC 664
                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Miller S., Shoback D., "Expression and signal transduction of calcium-sensing receptors in
                                                                                                                                                                                                                        409 F---VQEDKYLRL-----AIISFQGLCMLLDFVSMLVVYHFRKAKSIRASGLILLET
                                                                                                                                                                                                                                                                   458 ILFGSLLLYFPVVILYFEPSTFRCILLRWARLLGFATVYGTVTLKLHRVLKVFLSRTAQR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 256-600 FROM N.A. (ISOFORM A), AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY STRAIN=C57BL/6; TISSUE=Kidney;
MEDLINE=20092290; Pubmed=10625662;
                                                                                                 113275 MW; AB22AF2A28D9AOCF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -L., Chang W., Crumrine D., Koemueves L., Mauro T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM A), AND TISSUE SPECIFICITY.
STRAINB-Black Swiss X 129/SvJ; TISSUE-Kidney;
MEDLINE-20119279; PubMed-10652312;
Pi M., Garner S.C., Flannery P., Spurney R.F., Quarles L.D.;
"Sensing of extracellular cations in CasR-deficient osteoblasts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Epiphyseal cartilage;
MEDLINE=20043955; PubMed=10579354;
Chang W., Tu C., Chen T.-H., Komuves L., Oda Y., Pratt S.A.,
                                                                                                                               Length 999;
                                                                                                                                                       87; Indels
Transmembrane; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Evidence for a novel cation-sensing mechanism.";
J. Biol. Chem. 275:3256-3263(2000).
                                                                                                                                4.3%; Score 136; DB 1; 22.3%; Pred. No. 0.013;
                                                                                               N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                               ---IPYMTGGRVMRMLAVILLV--VFWFLI----GW 544
                                                                                                                                                                                                                                                                                                                                  783 PRFISPISOVVMTAMLAGVQLIGSLIWLSVVPPGW 817
                                                                                                                                                       44; Mismatches
          POTENTIAL.
POTENTIAL.
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POTENTIAL.
POTENTIAL.
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Endocrinology 140:5883-5893(1999).
  receptor;
                                                                                                                                Query Match 4.3
Best Local Similarity 22.3
Matches 48; Conservative
                    739
769
812
857
893
929
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Elias P.M., Bikle D.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse)
                                                                                    888
518
999 AA;
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InterPro; IPR001828; ANF_receptor.

AR InterPro; IPR001828; ANF_receptor.

R Ffam; PF001094; ANF_receptor; 1.

R Pfam; PF01094; ANF_receptor; 1.

R PRINTS; PR001948; GPCRMGR.

R PROSTTE; PS00980; G_PROTEIN_RECEP_F3_1; 1.

R PROSTTE; PS00981; G_PROTEIN_RECEP_F3_2; 1.

R PROSTTE; PS05259; G_PROTEIN_RECEP_F3_3; 1.

R PROSTTE; PS0529; G_PROTEIN_RECEP_F3_3; 1.

R PROSTTE; PS0529; G_PROTEIN_RECEP_F3_3; 1.

R PROSTTE; PS0529; G_PROTEIN_RECEP_F3_3; 1.

R PROSTTE; PS00981; G_PROTEIN_RECEP_F3_3; 1.

R PROST TESTER TE
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                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 646-799 FROM N.A., AND TISSUE SPECIFICITY.

MEDLINE-97231187; Pubmed-907682;

Quarles L.D., Hartle J.E. II, Siddhanti S.R., Guo R., Hinson T.K.;

A distinct cation-sensing mechanism in M3T3-El osteoblasts
J. Bone Miner. Res. 12:393-402(1997).

-!-FUNCTION: SENSES CHANGES IN THE EXTRACELLULAR CONCENTRATION OF
CALCIUM IONS. THE ACTIVATY OF THIS RECEPTOR IS MEDIATED BY A
G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
MESSENGER SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE PRODUCED BY ALTERNATIVE SPLICING.
-!- TISSUE SPECIFICITY: EPIDERMIS, KIDNEY AND CARTILAGE.
-!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
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VIOURINGE (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                       TISSUE=Kidney;
Moawad T.I., Riccardi D.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                      STRAIN=NMRI; TISSUE=Brain;
Hildenbrand J., Ammon H.P.T., Wahl M.A.;
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
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VII (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
VI (POTENTIAL).
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[4] SEQUENCE OF 507-582 FROM N.A. (ISOFORM A).
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SEQUENCE OF 562-814 FROM N.A.
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CARBOHYD
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NCBI_TaxID=10116;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Extracellular calcium-sensing receptor precursor (CaSR) (Parathyroid
                                                                                                                                                                                                                                                                                              --NLVPEFRGVMKVDINLQKVDIDQCSSDGWFSGTHKCHLNNS------ECMPIKG
                                                                                                                                                                                                                                                                                                               434 IYTCLPG-RGLF---TNGSCADIKKV--EAWQVLKHLRHLNFTNNMGEQVTFDECGDLVG
                                                                                                                                                                                                                                                                                                                                    LGFVL-----GAYECICKAG---FYHPGVLPVNNFRRGPDOHIS----
                                                                                                                                                                                                                                                                                                                                               AGTRKGIIEGEPTCCFECVECPDGEYSGETDASACDKCPDDFWSNENYTSCIAKEIEFLA
                                                                                                                                                                                                                                                                                                                                                                                                                        LYFEPSTFRCILLRWARLLGFATVYGTVTLKLHRVLKVFLSRTAQRIPYMTGGRVMRMLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            | | : | : | :: | :: | :: | FIGEPQDWTCRLRQPAFGISFVLCISCILVKTNRVLLVFEAKIPTSFHRKWWGLNLQFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     V-----ILLVVFWFLIGWTSSVCQNLEKQISLIGQGKTSDHLIFNMCLIDRWDYMTAV
                          (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                     DB 1; Length 1079;
                                                             A -> S (IN ISOFORM

A -> S (IN REF 2).

L -> P (IN REF 2).

G -> D (IN REF 2).

V -> A (IN REF 2).

Y -> H (IN REF 2).

Y -> H (IN REF 2).

E -> U (IN REF 5).

E -> U (IN REF 5).

L -> I (IN REF 5).

L -> I (IN REF 5).

U -> M (IN REF 2).

TGSN -> SGWI (IN REF 2).

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        (GLCNAC.
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11.7%; Pred. No. 0.019;
.ve 58; Mismatches 1
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1076 I ->
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CASR OR GPRC2A OR PCAR1.
Rattus norvegicus (Rat).
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Conservative 5
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                        MEDITINE 12341465; PubMed=7724534;

Ruat M., Snowman A.M., Snyder S.H.;

Ruat L., Snowman A.M., Snyder S.H.;

"Calcium sensing receptor: molecular cloning in rat and localization to nerve terminals.";

Proc. Natl. Acad. Sci. U.S.A. 92:3161-3165(1995).

-!- FUNCTION: SENSE CHANGES IN THE EXTRACELLULAR CONCENTRATION OF CALCIUM IONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR CALCIUM-SENSING RECEPTOR. EXTRACELLULAR (POTENTIAL).
                                             Riccardi D., Park J., Lee W., Gamba G., Brown E.M., Hebert S.C.; "Cloning and functional expression of a rat kidney extracellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PRO0248; GPCRMGR.
PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
PROSITE; PS00990; G_PROTEIN_RECEP_F3_2; 1.
PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
G_protein coupled receptor; Transmembrane; Glycoprotein; Signal.
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V (POTENTIAL).
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VII (POTENTIAL).
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N-LINKED (GLCNAC...) (PN
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STRAIN-Sprague-Dawley, TISSUE-Kidney outer medulla, MEDLINE-95116508; PubMed-7816802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       calcium/polyvalent cation-sensing receptor.";
Proc. Natl. Acad. Sci. U.S.A. 92:131-135(1995)
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EMBL; U20289; AAC52195.1; -.
InterPro; IPR001828; ANF_receptor.
InterPro; IPR000337; GFCR_Mgr.
Pfam; PF01094; ANF_receptor; 1.
                                                                                                                                                                    SEQUENCE OF 1-294 FROM N.A.
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and neonatal hyperparathyroidism."; J. Clin. Invest. 96:2683-2692(1995)
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                                                                                     Endocrinology 137:3842-3848(1996).
                                                                                                            SEQUENCE OF 643-908 FROM N.A. MEDLINE=96193893; PubMed=8613532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=96292293; PubMed=8675635;
                                                                                                                                                                                                           MEDLINE=94094324; PubMed=7916660;
                                                                                                                                                                                                                                                                                                                                                                                  Genet. 8:303-307(1994).
                                                                                                                                                                                                                                                                                                           VARIANT ADH ALA-127.
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 SEQUENCE FROM N.A.
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                                       Raue
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   18;
                                               235 HRRGPNQGPRGLGHSWRRKDGLGGDKSHFKWSPPYLECENGSYKPGWLVTLSSAIYGLQP 294
                                                                       377 HEEG --- GNRLLNSSTAFRPLCTGDENINSVETPYMDYEHLRISYNVYLAVYSIAHALQD 433
                                                                                                --NLVPEFRGVMKVDINLQKVDIDQCSSDGWFSGTHKCHLNNS------ECMPIKG 342
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                                                                                                                                                                                                                    AGTRKGIIEGEPTCCFECVECPDGEYSGETDASACDKCPDDFWSNENHTSCIAKEIEFLA 607
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                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CaSR) (Parathyroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Parathyroid;
MEDLINE=95279439; PubMed=7759551;
MEDLINE=95279439; PubMed=7759551;
MEDLINE=95279439; PubMed=7759551;
Habert J.E., Capuano I.V., Hammerland L.G., Hung B.C., Brown E.M., Hebert S.C., Nemeth B.F., Fuller F.;
"Molecular cloning and functional expression of human parathyroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aida K., Koishi S., Tawata M., Onaya T.;
"Molecular cloning of a putative Ca(2+)-sensing receptor cDNA from
human kidney.";
                                                                                                                      434 IYTCLPG-RGLF---TNGSCADIKKV--EAWQVLKHLRHLNFTNNMGEQVTFDECGDLVG
                                                                                                                                             343 LGFVL-----GAYECICKAG---FYHPGVLPVNNFRRGPDQHIS----
                                                                                                                                                                     NYSIINWHLSPEDGSIVFKEVGYYNVYAKKGERLFINEEKILWSGFSREVPFSNCSRDCQ
                                                                                                                                                                                            380 -GSTKDVSEE----AYVCLPCREG------CPFCADD-----SPCFVQEDKYLR
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 Length 1079;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pearce S.H.S., Thakker R.V.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CASR_HUMAN STANDARD; PRT; 1078 AA.
P41180; Q13912; Q16379; Q16108; Q16109; Q16110;
O1-FEB-1995 (Rel. 31, Created)
O1-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Extracellular calcium-sensing receptor precursor
Cell calcium-sensing receptor).
4.2%; Score 133.5; DB 1;
21.7%; Pred. No. 0.023;
iive 58; Mismatches 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Biochem. Biophys. Res. Commun. 214:524-529(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   calcium receptor cDNAs.";
J. Biol. Chem. 270:12919-12925(1995).
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                         Conservative
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                      93;
  Query Match
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SEQUENCE OF 1-61 FROM N.A., AND VARIANT FHH ALA-39.
MEDLINE-95403641; PubMed=7673400;
Aida K., Koishi S., Inoue M., Nakazato M., Tawata M., Onaya T.;
Aifan Hypocalcuiutchypercalcemia associated with mutation in the human Ca(2+1)-sensing receptor gene.";
J. Clin. Endocrinol. Metab. 80:2594-2598(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-95179179; PubMed-7874174; Pollak M.R., Erom B.M., Esch D.N., Rifor O., Park J., Pollak M.R., Erom B.M., Estep H.L., McLaine P.N., Kifor O., Park J., Soldman C.E., Seldman J.G.; "Autosomal dominant. hypocalcaemia caused by a Ca(2+)-sensing receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Calcium-sensing receptor mutations in familial benign hypercalcemia
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Ward B.K., Stuckey B.G.A., Gutteridge D.H., Laing N.G., Pullan P.T.,
Ratajczak T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Bikle D.D., Ratnam A., Mauro T., Harris J., Pillai S.; "Changes in calclum responsitiveness and handling during keratinocyte differentiation. Potential role of the calcium receptor."; J. Clin. Invest. 97:1085-1093(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pollak M.R., Brown E.M., Chou Y. H.W., Hebert S.C., Marx S.J., Steinmann B., Levi T., Seidman C.E., Seidman J.G.; "Mutations in the human Ca(2+)-sensing receptor gene cause familial hypocalciuric hypercalcemia and neonatal severe cell 75:1297-1303(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VELTANTS FHH MET-62; CYS-66; MET-138; GLU-143 AND GLN-227.
MEDLINE-95243222; PubMed-7726161;
Chou Y.-H.W., Pollak M.R., Brandi M.L., Toss G., Arnqvist H.,
Atkinson A.B., Papapoulos S.E., Marx S., Brown E.M., Seidman J.G.,
MEDLINE-96343808; PubMed-8756555;
Freichel M., Zink-Lorenz A., Holloschi A., Hafner M., Flockerzi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seidman C.E.; the human Ca(2+)-sensing-receptor gene that cause familial hypocalciuric hypercalcemia."; Am. J. Hum. Genet. 56:1075-1079(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANTS ADHP THR-116; HIS-681 AND SER-806, AND VARIANT SER-851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=96311554; PubMed=8733126;
Baron J., Winer K.K., Yanovski J.A., Cunningham A.W., Laue L.,
Zimmerman D., Cutler G.B. Jr.,
"Mutations in the Ca(2+)-sensing receptor gene cause autosomal
dominant and sporadic hypoparathyroidism.";
Hum. Mol. Genet. 5:601-606(1996).
                                                                                                                                "Expression of a calcium-sensing receptor in a human medullary thyroid carcinoma cell line and its contribution to calcitonin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A novel mutation (L174R) in the Ca2+-sensing receptor gene associated with familial hypocalciuric hypercalcemia."; Hum. Mutat. 10:233-235(1997).
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VARIANTS FHH GLN-185; LXS-297 AND TRP-795.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISEASE: DEFECTS IN CASR ARE ALSO THE CAUSE OF AUTOSOMAL DOMINANT HYPOCALCEMIA (ADH) IN WHICH THE RECEPTOR IS ACTIVATED AT SUBNORMA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISEASE: DEFECTS IN CASR ARE ALSO THE CAUSE OF AUTOSOMAL DOMINANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOPARATHYROIDISM (ADHP). ADHP IS CHARACTERIZED BY HYPOCALCEMIA AND HYPERPHOSPHATEMIA DUE TO INADEQUATE SECRETION OF PARATHYROID HORMONE. SYMPTOMS ARE SEIZURES, TETANY AND CRAMPS. SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R MIM; DULLYS; ...
R InterPro; IPR001828; ANF_receptor.
R InterPro; IPR001837; GPCR_MGr.
R Ffam; PF00003; 7tm_3; 1.
R Ffam; PF00004; ANF_receptor; 1.
R Pfam; PF00004; ANF_receptor; 1.
R PROSITE; PS00949; G_PROTEIN_RECEP_F3_1; 1.
R PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
R PROSITE; PS00980; G_PROTEIN_RECEP_F3_3; 1.
R PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
R PROSITE; PS50259; G_PROTEIN_RECEP_F3_5; 1.
R PROSITE; PS50259; G_PROTEIN_RECEP_F3_6; 1.
R PROSITE; PS5025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR CALCIUM-SENSING RECEPTOR
                                                                                                                                                   CALCIUM IONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
                                                                                                                                             -!- FUNCTION: SENSE CHANGES IN THE EXTRACELLULAR CONCENTRATION OF CALCIUM IONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A
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                                                 Nakayama T., Minato M., Nakagawa M., Soma M., Tobe H., Aol N
Kosuge K., Sato M., Ozawa Y., Kanmatsuse K., Kokubun S.;
"A novel mutation in Ca2+-sensing receptor gene in familial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S68032; AAB29413.2; ALT_SEQ. S68033; AAB29414.1; -. S68005; AAB29415.1; -. S81755; AAD14370.1; -.
                                  MEDLINE-21603857; PubMed=11762699;
                                                                                                          hypocalciuric hypercalcemia.";
Endocrine 15:277-282(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X81086; CAA56990.1; -. EMBL; U20759; AAA86503.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  U20760; AAA86504.1; -. D50855; BAA09453.1; -. S83176; AAB46873.1; -. S79217; AAB35262.2; -.
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MIM; 601198;
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311 QKVDIDQCSSDGWFSGTHKC---HLNNSE-CMPIKGLGFVLGAYECICKAG---FYHPGV 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                         364 LPVNNFRRRGPDQH-----ISGSTKDVSEE----AYVCLPCREG-------CPFCAD 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                           D-----SPCFVQEDKYLR-----LAIISFQGLCMLLDFVSMLVVYHFRKAKSIRASG 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               588 DFWSNENHTSCIAKEIEFLSWTEPFGIALTLFAVLGIFLTAFVLGVFIKFRNTPIVKATN 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            452 LILLETILFGSLLLYFPVVILYFEPSTFRCILLRWARLLGFATVYGTVTLKLHRVLKVFL 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CASR_BOVIN STANDARD; PRT; 1085 AA. p35384; 01-JUN-1994 (Rel. 29, Created) 01-JUN-1994 (Rel. 29, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Extracellular calcium-sensing receptor precursor (CaSR) (Parathyroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     512 SRTAQRIPYMTGGRVMRMLAV-----ILLVVFWFLIGWTSSV-CQNLEKQISLI----
                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                  Score 127; DB 1; Length 1078; Pred. No. 0.072;
                                                                                                                                                                                                                                                                                                                                                48; Mismatches 139; Indels
                                                                                                                                               CYTOPLASMIC (POTENTIAL).
VI (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
VII (POTENTIAL).
                                           II (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                     EXTRACELLULAR (POTENTIAL).
V (POTENTAR.)
EXTRACELLULAR (POTENTIAL).
                                                                         III (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                               (POTENTIAL).
               (POTENTIAL)
                               CYTOPLASMIC
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CASR OR GPRC2A OR PCAR1.
                                                                                                                                                                                                                                                                                                                   4.0%;
                                                                                                                                                                                                                                                                                                                                                71; Conservative
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 Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
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Genew;
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                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             476 EQVTFDEC---GDLAGNYSIINWHLSPEDGSIVFKEVGY----YNVYAKKGERLFINDEK 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR CALCIUM-SENSING RECEPTOR. EXTRACELLULAR (POTENTIAL).
                        FUNCTION: SENSE CHANGES IN THE EXTRACELLULAR CONCENTRATION OF CALCIUM IONS. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND
                                                                                                                                                               SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS
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INKED (GLCNAC. . .) (POTENTIAL)
5D66DE8C9CD13E47 CRC64;
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V (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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VII (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001828; ANF receptor.
InterPro; IPR000337; GPCR_Mgr.
Pfam; PP00003; 7tm_3; 1.
PRINTS; PR00248; GPCRMGR.
PROSITE; PS00099; G_PROTEIN_RECEP_F3_1; 1.
PROSITE; PS00090; G_PROTEIN_RECEP_F3_2; 1.
PROSITE; PS00981; G_PROTEIN_RECEP_F3_2; 1.
PROSITE; PS00981; G_PROTEIN_RECEP_F3_2; 1.
PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  452 LILLETILFGSLLLYFPVVILYFEPSTFRCILLRWARLLGFATVYGTVTLKLHRVLKVFL 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Integral membrane protein.
-!- TISSUB SPECIFICITY: WIDELY EXPRESSED IN DIFFERENT REGIONS OF THE ADULT BRAIN AS WELL AS IN FETAL BRAIN.
-!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
STRONGEST, TO MGLUR3.
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H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Molecular cloning, functional expression and pharmacological characterization of the human metabotropic glutamate receptor type
                                                                               RELSYLLLFSLLCCFSSSLFFIGEPQDWTCRLRQPAFGISFVLCISCILVKTNRVLLVFE
                                                           512 SRTAQRIPYMTGGRVMRMLAVILLVVFWFLIG--WTSSVCONLEKQISLIGOGKTSDHLI
                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Flor P.J., Lindauer K., Puttner I., Ruegg D., Lukic S., Knopfel
Kuhn R.;
                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butelo
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                               Metabotropic glutamate receptor 2 precursor (mGluR2).
GRM2 OR GPRC1B OR MGLUR2.
                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                   872 AA
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PROSITE; PS00979; G_PROTEIN_RECEP_F3_1;
PROSITE; PS00980; G_PROTEIN_RECEP_F3_2;
PROSITE; PS00981; G_PROTEIN_RECEP_F3_3;
PROSITE; PS50259; G_PROTEIN_RECEP_F3_4;
                                                                                                                                                                                                                                    PRT;
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InterPro; IPR000337; GPCR_Mgr.
Pfam; PF00003; 7tm_3; 1.
Pfam; PF01094; ANE_receptor; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eur. J. Neurosci. 7:622-629(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=95346007; Pubmed=7620613;
                                                                                                                                                                                                                               MGR2_HUMAN STANDARD;
014416; Q9H3N6;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BAB19817.1;
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                                                                                                                                                                                                                                                                                                (Rel. 41,
                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
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                                                                                                                       570 FNMC 573
                                                                                                                                                     FITC 766
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                   MAY MEDIATE SUPPRESSION OF NEUROTRANSMISSION OR MAY BE INVOLVED IN SYNAPTICE STABILIZATION.
SYNAPTICE STABILIZATION.
SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: IS WIDELY DISTRIBUTED IN THE CNS AND PROMINENT EXPRESSION IS SEEN IN GOLGI CELLS OF THE CEREBELLUM AND SOME PARTICULAR NEURONAL CELLS IN OTHER BRAIN REGIONS.
SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
STRONGEST, TO MGLURA.
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  MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DR PIR; JH0561; JH0561.

DR InterPro: IPR001828; ANF_receptor.

DR InterPro: IPR00033; Tem_3; dpcR_Mgr.

DR Pfam; PF00003; 7tm_3; dpcR_Mgr.

DR Pfam; PF01094; ANF_receptor; 1.

DR PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.

DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_2; 1.

DR PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.

DR PROSITE; PS00481; G_PROTEIN_RECEP_F3_4; 1.

TR SIGNAL IN POTENTIAL
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EXTRACELLULAR (POTENTIAL).

VII (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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"A family of metabotropic glutamate receptors.";
Neuron 8:169-179(1992).
-i- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2010 (Rel. 40, Last annotation update)
Metabotropic glutamate receptor 2 precursor (mGluR2).
GRM2 OR GPRCIB OR MGLUR2.
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                                                                                                                                                                                                                477
  ---IGRYN 454
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SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS
                                        352 CIC-----RAGFYHPGVLPVNNF------RRRGPDQHISGSTKDVSE
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                                                                                                                         388 E---AYVCLPCREGCPF-----CADD-----SPCFVQEDKYLR-----
                                                                                                                                                                      GEVCCWLCIPCO - - - PYEYRLDEFTCADCGLGYWPNASLTGCFELPQEYIRWGDAWAVGP
                                                                                                                                                                                                                LAIISFQGLCMLLDFVSMLVVYHFRKAKSIRASGLILLETILFGSLLLYFPVVILYFEPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stephan D., Bon C., Holzwarth J.A., Galvan M., Pruss R.M.; "Human metabotropic glutamate receptor 1: mRNA distribution, chromosome localization and functional expression of two splice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGRI_HUMAN STANDARD; PRT; 1194 AA. 013255; Q13256; Q14757; Q14758; Q9UGT0; Q9UGS9; Q9NU10; Q1-NOV-1997 (Rel. 35, Last sequence update) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) metabotropic glucamate receptor I precursor (mGluR1). GRM1 OR GPRCIA OR MGLURI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bates K.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
415 GRRLYKDFVLNVKFDAPFRPADTDDEVRFDRFGDG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neuropharmacology 35:1649-1660(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pharmacol. 48:648-657(1995)
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MGRI_HUMARN
AC 013255,
DT 01-NOV.
DT 15-JUNV
DT 11-JUNV
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
NSUGKSVASPEGGOVPKG -> KKRQPEFSPSSOCPSAH
MISSING (IN ISOPORM BETA).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----CPFC-----ADDSPCFVQEDKYLR-----LAIISFQGLCMLLDFVSMLVV 438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    615 VLYRDTPVVKSSSRELCYIILAGIFLGYVCPFTLIAKPTTTSCYLQRLLVGLSSAMCYSA 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     498 GTWHEGVLNIDDYKIQ---MNKSGVVRSVCSEPCLKGQIKVIRKGEVSCCWICTACKENE 554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44; Gaps
                                                                                                                                                                                                                                                                               Primm; PF01094; ANF_receptor; 1.
PRINTS; PR00248; GPCRMGR.
PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
G-PROTIE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal; Multigene family; Alternative splitcing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METABOTROPIC GLUTAMATE RECEPTOR 1. EXTRACELLULAR (POTENTIAL).
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P -> S (IN REF. 3).
W; 970E51AF40584F40 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      V (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
VI (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 II (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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SER-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLN/PRO-RICH.
GLN/PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 116;
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                                                                                                                                                                                                                                      InterPro; IPR001828; ANF_receptor
EMBL, U31215, AAA87843.1; -.
EMBL, 131216, AAA87844.1; -.
EMBL, L76631; AAB05337.1; -.
EMBL, L76631; AAB05338.1; -.
EMBL, AL098667; CAB75694.1; -.
EMBL, AL035698; CAB65991.1; -.
EMBL, AL035699; CAB65991.1; -.
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98619 MW; 66F28663CE35F740 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1991 (Rel. 20, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Metabotropic glutamate receptor 1 precursor (MG1uR1).
GRM1 OR GFRCIA OR MGLURI.
                          DB 1;
                          3.6%; Score 115.5; DE 18.6%; Pred. No. 0.43; iive 72; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 1199 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92022526; PubMed=1656524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1991 (Rel. 20, Created)
                                     Local Similarity 18.6
nes 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
877 AA;
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SEQUENCE FROM N.A.
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P23385;
  SEQUENCE
                          Query Match
                                                                                                   272
                                                                                                                                                                                                                                                      412
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                                                   Matches
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                                                                                                                                                                                                                                                                glutamate receptor type 3.",
Brain Res. Mol. Brain Res. 40:55-63(1996).
-!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR
IS MEDIATED BY A G-PROTEIN THAT INHIBITS ADENYLATE CYCLASE
                                                                                                                                                                                                                                         Makoff A., Volpe F., Lelchuk R., Harrington K., Emson P.;
"Molecular characterization and localization of human metabotropic
                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Integral membrane protein. SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS
                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro: IPR000337; GPCR_Mgr.

Ffam; PF01003, 7tm_3; 1.

Ffam; PF01094; ANF_receptor; 1.

PR01249; GPCRMGr.

PROSTTE; PS00249; GPCRMGr.

PROSITE; PS00999; G_PROTEIN_RECEP_F3_1; 1.

PROSITE; PS00991; G_PROTEIN_RECEP_F3_2; 1.

PROSITE; PS50259; G_PROTEIN_RECEP_F3_2; 1.

PROSITE; PS50259; G_PROTEIN_RECEP_F3_3; 1.

PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Signal; Multigene family.
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N-LINKED GLCNAC. .) (POTENTIAL).
N-LINKED GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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                                                                        01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Metabotropic glutamate receptor 3 precursor (mGluR3),
GRM3 OR GPRCIC OR MGLUR3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                 877 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                               TISSUE=Brain;
MEDLINE=96437205; PubMed=8840013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X77748; CAA54796.1; -.
                                                                                                                                                                                                                                                                                                                                                        STRONGEST, TO MGLUR2.
                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HGNC: 4595; GRM3
                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                   SEQUENCE FROM N.A.
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687
708
733
755
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CARBOHYD
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                                                                                                                                                              138 VMLQSNKSRE----QNLQDDLDWYQALVW----SLLEGEPSISRAAITFSTDSLSAPAP 188
                                                                                                                                                                                                                                                                                                                             189 QVFLQATREESRIILLQDLSSSAPHLANATLETEWFHGLRRKWRPHLHRRGPNQGPRGLGH 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NTTKLCDAMKI-LDGKKLYKDYLLKIN-FTAPFNPNKDADSIVKFDTFGDGMGRYNVFNF 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          470 QNVGGKYSYLKVGHWAETLSLDVNSIHWSRNSVPTSQCSDPCAPNEMKNMQPGDVCCWIC 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  427 CMLLDFVSMLVVYHFRKAKSIRASGLILLETILFGSLLLYFPVVILYFEPSTFRCILLRW 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 487 ARLLGFATVYGTVTLKLHRVLKVF--LSRTAQRIPYMT-GGRVMRMLAVIL----LVVFW 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWRRK--DGLGGDKSHFKWSPPYLECENGSYKP-----GWLVTLSSAIYGLQPNLVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----CKAGFYHPGV-LPVNNF---RRRGPDQHIS-----GSTKDVSEE---AYVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               393 LPCRE------GCPFC-----ADDSPCFVQEDKYLR------LAIISFQGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               590 CMV-----VTVFIKHNNTPLVKASGRELCYILLFGVGLSYCMTFFFIAKPSPVICALRRL
                                                                                                                                                                                                                                                                                                                                                                                                          ----OPVROFDR-YFQSLNPYNNH------RNPWFRDF-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---EFRGVMKVDINLQKVDIDQCSSDGWFSGTHKCHLNNSECMPIKGLGFVLGAYECI--
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Length 877;
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MEDLINE=93343913; PubMed=7688218;
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                                                                                                                                                                       1199 AA; 133235
                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
 1034
1080
11135
1199
98
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397
515
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897
1199
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                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                             515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-2002
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VARSPLIC
SEQUENCE
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CARBOHYD
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The pin J.-P., Waeber C., Prezeau L., Bockaert J., Heinemann S.F.;

The Alternative splicing generates metabotropic glutamate receptors inducing different patterns of calcium release in Xenopus ocytes.";

Proc. natl. Acad. Sci. U.S.A. 89:1031-10335(1992).

-!- FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL.

CALCIUM SECOND MESSENGER SYSTEM. MAY PARTICIPATE IN THE CENTRAL ACTION OF GLUTAMATE IN THE CR.S. SUCH AS LONG-TERM POPENTIATION IN C. IS UBCELLULAR LOCATION: Integral membrane protein.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- ALTERNATIVE PRODUCTS: 3 ISOFORMS; IA (SHOWN HERE), ARE PRODUCED BY ALTERNATIVE SPLICING. 1B AND 1C ARE C-TERMINALLY TRUNCATED FORMS OF 1A.

-!- TISSUE SPECIFICITY: IS PREDOMINANTLY EXPRESSED IN CEREBELLAR PURKING CELLS, CA2-CA3 PYRAMIDAL CELLS OF THE IIPPOCAMPUS, AND MITRAL AND TUFFED CELLS OF THE OLFACTORY BULB.
                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                           MISCELLANEOUS: ACTIVATED BY QUISQUALATE > GLUTAMATE > IBOTENATE > TRANS-1- AMINOCYCLOPENTYL-1,3-DICARBOXYLATE; INHIBITED BY 2-AMINO- 3-PHOSPHONOPROPIONATE.
                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS. STRONGEST, TO MGLURS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0248; GPCENGR.

PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.

PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.

PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.

PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein; Signal; Multigene family; Alternative splicing.
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EXTRACELLULAR (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VI (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                     Tanabe Y., Masu M., Ishii T., Shigemoto R., Nakanishi
"A family of metabotropic glutamate receptors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001828; ANF receptor.
InterPro; IPR000337; GPCR_Mgr.
Pfam; PF00003; 7tm_3; 1.
                                                                                         ALTERNATIVE SPLICING (ISOFORM 1C)
                                                                                                       TISSUE=Brain;
MEDLINE=93066232; PubMed=1438218;
ALTERNATIVE SPLICING (ISOFORM 1B)
                       MEDLINE-92110002; PubMed-1309649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01094; ANF_receptor; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X57569; CAA40799.1; -. EMBL; M61099; AAA19497.1; -. EMBL; S48085; AAB24138.1; -.
                                                                Neuron 8:169-179(1992).
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PIR; A41939; A41939.
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TRANSMEM
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
NSNRXVSWEBPGGRAPKG -> KKRQPEFSPSSQCPSAH
AQL (IN ISOFORM 1B).
MISSING (IN ISOFORM 1B).
SNGKSVGWSE -> FALDRQNTVY (IN ISOFORM 1C).
MISSING (IN ISOFORM 1C).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GEYHPGVLPVNNFRRRGPDQHISGSTKDVSEE-------AYVCLPCREG- 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----CPFC-----ADDSPCFVQEDKYLR-----LAIISFQGLCMLLDFVSMLVV 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                615 VLYRDTPVVKSSSRELCYIILAGIFLGYVCPFTLIAKPTTTSCYLQRLLVGLSSAMCYSA 674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTWHEGVLNIDDYKIQ---MNKSGMVRSVCSEPCLKGQIKVIRKGEVSCCWICTACKENE 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----FLSRTAQRIPYMTGGRVMRMLAVILLVVFWFLIGW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         439 YHFRKAKSIRASGLILLETILFGSLLLYFPVVILYFEPSTFRCILLRWARLLGFATVYGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               675 LVTKTNRIARILAGSKKKICTRKPRFMSAWAQVIIASILISVQLTLVVTLII-----
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Minakami R., Katsuki F., Sugiyama H.; "A variant of metabotropic glutamate receptor subtype 5: an evolutionally conserved insertion with no termination codon."; Biochem. Biophys. Res. Commun. 194:622-627(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 115; DB 1; Length 1199;
Pred. No. 0.71;
45; Mismatches 108; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Katsuki F.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Metabotropic glutamate receptor 5 precursor (mGluR5). GRM5 OR GPRC1E OR MGLUR5.
                      ASP/GLU-RICH (ACIDIC).
SER-RICH.
                                                                                                     N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Rel. 32, Created)
(Rel. 34, Last sequence update)
(Rel. 41, Last annotation update)
GLN/PRO-RICH
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KVDIDQCSSDGWFSGTHKCHLNNSECMPIKGLGFVLGAYECICKAGFYHPGVLPVNNFRR 371
                                                                                                                                                                                                                                                                                                                                                      PRT;
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PIR; JH0562; JH0562.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92110002; PubMed=1309649;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria; Rodentia;
                                                              RGPDOHI - - - - SGSTKDVSEE - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRONGEST, TO MGLUR2.
                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neuron 8:169-179(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16;
FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
               MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM AND GENERATES A CALCIUM-ACTIVATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSLTLKTHHVQDSKMGFVINAIYSMAYGLHNMQMSLCPGYAGLCDAMKPIDGRKLLESLM 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ETEWFHGLRRKWRPHLHRRGPNQGPRGLGHSWR-----RKDGLGGDKSHFKWSPPYLECE 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVKWFDDYYLKLRPETNHRNP-----WFQEFWQHRFQCRLEGFPQENSKYNKT-----CN 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NG------SYKPGWLV-TLSSAIYGL---QPNLVPEFRGV-------MKVDINLQ 311
                                                                                           OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                       SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
                                                          SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; 5A (SHOWN HERE) AND 5B; ARE
PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER BY AN INSERTION
32 RESIDUES.
                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001828; ANF_receptor.
InterPro; IPR000337; GPCR_Mgr.
Pfam; PF000037; Trm_3: 1.
Pfam; PF000037; Trm_3: 1.
Pfam; PF00004; ANF_receptor; 1.
PR01054; ANF_receptor; 1.
PR05ITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
PR05ITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
PR05ITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
PR05ITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; Signal; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VII (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METABOTROPIC GLUTAMATE RECEPTOR 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A3C73606681C6A25 CRC64;
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
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ive 53; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 114;
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                                                                                                                                                                                                                                                                                       EMBL; D28538; BAA05891.1; -. EMBL; D28539; BAA05892.1; -. EMBL; S64316; AAD13954.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.68;
                                                                                                                                       STRONGEST, TO MGLUR1.
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1212
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nes 80; Conserv
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SEQUENCE
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KTNFTGVSGDTILFDENGDSPGRYEIMNFKEMG------KDYFDYINVGSWDNGEL 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
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TISSUE SPECIFICITY: IS WIDELY DISTRIBUTED IN THE CNS. PREDOMINAN
ENTRESSION IS SEEN IN THE NEURONAL CELLS OF THE CEREBRAL CORTEX,
DENTRYE GYRUS, AND GLIAL CELLS THROUGHOUT BRAIN REGIONS.
SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
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                                                                                 ----AYVCLPCREG-----CPFC
                                                                                                                                                             493 KMDDDEVWSKKSNIIRSVCSEPCEKGQIKVIRKGEVSCCWTCTPCKENEYVFDEYTCKAC
                                                                                                                                                                                                                                                   -----ADD-SPCFVQEDKYLR-----LAIISFQGLCMLLDFVSMLVVYHFRKAKSIRA
                                                                                                                                                                                                                                                                                                  SGLILLETILFGSLLLYFPVVILYFEPSTFRCILLRWARLLGFATVYGTVTLKLHRVLKV
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Pfam; PF01004; ANF_receptor.
Pfam; PF01094; ANF_receptor; 1.
PRINTS; PR01024; ANF_receptor; 1.
PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
PROSITE; PS50259; G_PROTEIN_RECEP_F3_3; 1.
PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
C_Protein coupled receptor; Transmembrane; Glycoprotein; Signal; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nakanishi S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Metabotropic glutamate receptor 3 precursor (mGluR3).
6RM3 OR GFRCIC OR MGLUR3.
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tanabe Y., Masu M., Ishii T., Shigemoto R., Nal
"A family of metabotropic glutamate receptors."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        879 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |: ::| ||: : 673 -LAGSKKKICTKKPRFMSACAQLVIAFILICI 703
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                                                                                                                                                                                                                                                                                                                                                                            703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Abe T., Sugihara H., Nawa H., Shigemoto R., Mizuno N., Nakanishi S., "Molecular characterization of a novel metabotropic glutamate receptor mGluR5 coupled to inositol phosphate/Ca2+ signal
                                                                                                                                                                                                                                                                      390 YVCLPCRE------GCPFC-----ADDSPCFVQEDKYLR-----LAIISF
                                                                                                                                                                                                                                                                                  424 QGLCMLLDFVSMLVVYHFRKAKSIRASGLILLETILFGSLLLYFPVVILYFEPSTFRCIL
                                                                                                                                                                                                                                                                                                                           589 LCTCIVI-----TVFIKHNNTPLVKASGRELCYILLFGVSLSYCMTFFFIAKPSPVICAL
                                                                                                                                                                                                                                                                                                                                                      484 LRWARLLGFATVYGTVTLKLHRVLKVF--LSRTAQRIPYMT-GGRVMRMLAVIL----LV
                                                                                                                                                                                                                                                                                                                                                                   VII (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                   38;
 METABOTROPIC GLUTAMATE RECEPTOR 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=93343913; PubMed=7688218;
Minakami R., Katsuki F., Sugiyama H.;
"A variant of metabotropic glutamate receptor subtype 5: an
evolutionally conserved insertion with no termination codon.";
Biochem. Biophys. Res. Commun. 194:622-627(1993).
                                                                                                                                                                                                                              3.5%; Score 112; DB 1; Length 879; 22.6%; Pred. No. 0.8;
                                                                                                                                                                                                                                                 76; Indels
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                                                                                IV (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                  EXTRACELLULAR (POTENTIAL)
         EXTRACELLULAR (POTENTIAL) I (POTENTIAL).
                                         II (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                         3E5965EDD5E6DEED CRC64;
                                                          III (POTENTIAL),
CYTOPLASMIC (POTENTIAL),
IV (POTENTIAL),
                                                                                                              CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1993 (Rel. 26, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Metabotropic glutamate receptor 5 precursor (mGluR5).
GRM5 OR GPRCIE OR MGLUR5.
                              CYTOPLASMIC (POTENTIAL) II (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1203 AA
                                                                                                     V (POTENTIAL).
                                                                                                                          (POTENTIAL)
                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92317054; PubMed=1320017;
                                                                                                                                                                                                                                                  30;
                                                                                                                                                                                                          98959 MW;
                                                                                                                                                                                                                            uery Match 3.5 est Local Similarity 22.6 atches 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat)
                                                                                                                                                                                   414
439
879 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                               537 VFWFLI 542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transduction.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Brain;
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P31424;
                              DOMAIN
TRANSMEM
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TRANSMEM
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                                                                                                                                                                                                         SEQUENCE
                   FRANSMEM
                                                            FRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
FUNCTION: RECEPTOR FOR GLUTAMATE. THE ACTIVITY OF THIS RECEPTOR IS
                                     CALCIUM SECOND MESSENGER SYSTEM AND GENERATES A CALCIUM-ACTIVATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NG-----SYKPGWLV-TLSSAIYGL---QPNLVPEFRGV------MKVDINLQ 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                           QF
                                                                                                                                                              -!- TISSUE SPECIFICITY: WIDELY DISTRIBUTED IN NEURONAL CELLS OF THE CENTRAL NERVOUS SYSTEM.
-!- MISCELLANEOUS: ACTIVATED BY QUISQUALATE > GLUTAMATE > IBOTENATE
                                                                                                                                                                                                                                TRANS-1- AMINOCYCLOPENTYL-1, 3-DICARBOXYLATE.
-!- SIMILARITY: BELONGS TO FAMILY 3 OF G-PROTEIN COUPLED RECEPTORS.
                                                                             SUBCELLULAR LOCATION: Integral membrane protein.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; 5A (SHOWN HERE) AND 5B; ARE
PRODUCED BY ALTERNATIVE SPLICING. THEY DIFFER BY AN INSERTION
                   MEDIATED BY A G-PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00094; ANF_ECCEPTOR; 1.
PRINTS; PR00248; GFCKMGR.
PROSITE; PS00940; G_PROTEIN_RECEP_F3_1; 1.
PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1.
PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
G-PROTEIN_RECEP_F3_4; 1.
Multigene family; Alternative splicing.
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Pred. No. 1.5;
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EXTRACELLULAR (POTENTIAL).
VII (POTENTIAL).
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N.LINKED (GLCNAC. . .) (PO
M.SING (IN ISOPORM 5A).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (PO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D10891; -; NOT_ANNOTATED_CDS
EMBL; S64315; AAB27666.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001828; ANF_receptor.
InterPro; IPR000337; GPCR_Mgr.
Pfam; PF00003; 7tm_3; 1.
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                                                                                                                                                                                                                                                                            STRONGEST, TO MGLUR1.
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SEQUENCE
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RESULT 15 NRG2\_RAT

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                                                              BRAIN AND THYMUS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
  ESPECIALLY THE OLFACTORY BULB AND CEREBELLUM WHERE IT LOCALIZES IN GRANULE AND PURKINJE CELLS. IN THE HIPPOCAMPUS, FOUND IN THE GRANULE CELLS OF THE DENTRATE GYRUS. IN THE BASAL FOREBRAIN, FOUND IN THE CHOLINEGIC CELLS. IN THE HINDBRAIN, WEAKLY DETECTABLE IN THE MOTOR TRIGEMINAL NUCLEUS. NOT DETECTED IN THE HYPOTHALAMUS.
                                                                          403
                                                                                                 558
                                                                                                                         456
                                                                                                                                                                                        NRG2_RAT STANDARD; PRT; 868 AA.
035569; 035570; 035571; 035572; 035073;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Pro-neuregulin-2 precursor (Pro-NRG2) [Contains: Neuregulin-2 (NRG-2) (Neural-and thymus-derived activator for ERBB kinases) (NTAK)].
382 SSLTLRTHHVQDSKMGFVINAIYSMAYGLHNMQMSLCPGYAGLCDAMKPIDGRKLLDSLM 441
                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'A novel brain-derived member of the epidermal growth factor family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Higashiyama S., Horikawa M., Yamada K., Ichino N., Nakano N.,
Nakagawa T., Miyagawa J., Matsushita N., Nagatsu T., Taniguchi N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----NNFRRGPDQHI-SGSTKDVSEE----AYVCLPCREG-----CPFC----A
                                                                                                499 WSKKNNIIRSVCSEPCEKGQIKVIRKGEVSCCWTCTPCKENEYVFDEYTCKACQLGSWPT
                                                                                                                         DD-SPCFVQEDKYLR-----LAIISFQGLCMLLDFVSMLVVYHFRKAKSIRASGLILLE
                                                                                                                                       || : | : :|| | : | | :| | :| | DLITGCDLIPVQYLRWGDPEPIAAVVFACLGLLATLFVTVIFIIYRDTPVVKSSSRELCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 128-162, AND ALTERNATIVE SPLICING.
                         312 KVDIDQCSSDGWFSGTHKCHLNNSECMPIKGLGFVLGAYECICKAGFYHPGVLPV----
                                                442 KTNFTGVSGDMILFDENGDSPGRYEIMNFKEMG----KDYFDYINVGSWDNGELKMDDDEV
                                                                                                                                                                       457 TILFGSLLLYFPVVILYFEPSTFRCILLRWARLLGFATVYGTVTLKLHRVLKVFLSRTAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPLICING. THE ALPHA-TYPE AND BETA-TYPE DIFFER IN THE EGF-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97311397; PubMed-9168114;
Chang H., Riese D.J. II, Gilbert W., Stern D.F., McMahan U.J.;
"Ligands for ErbB-family receptors encoded by a neuregulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY: EXPRESSED IN MOST PARTS OF THE BRAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            that interacts with ErbB3 and ErbB4."; J. Biochem. 122:675-680(1997).
                                                                                                                                                                                                                        517 RI----PYMTGGRVMRMLAVILLVV 537
                                                                                                                                                                                                                                               678 KICTKKPRFMSACAQLVIAFILICI 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98006324; PubMed=9348101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 387:509-512(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                              NRG2 OR NTAK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ishiguro H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene."
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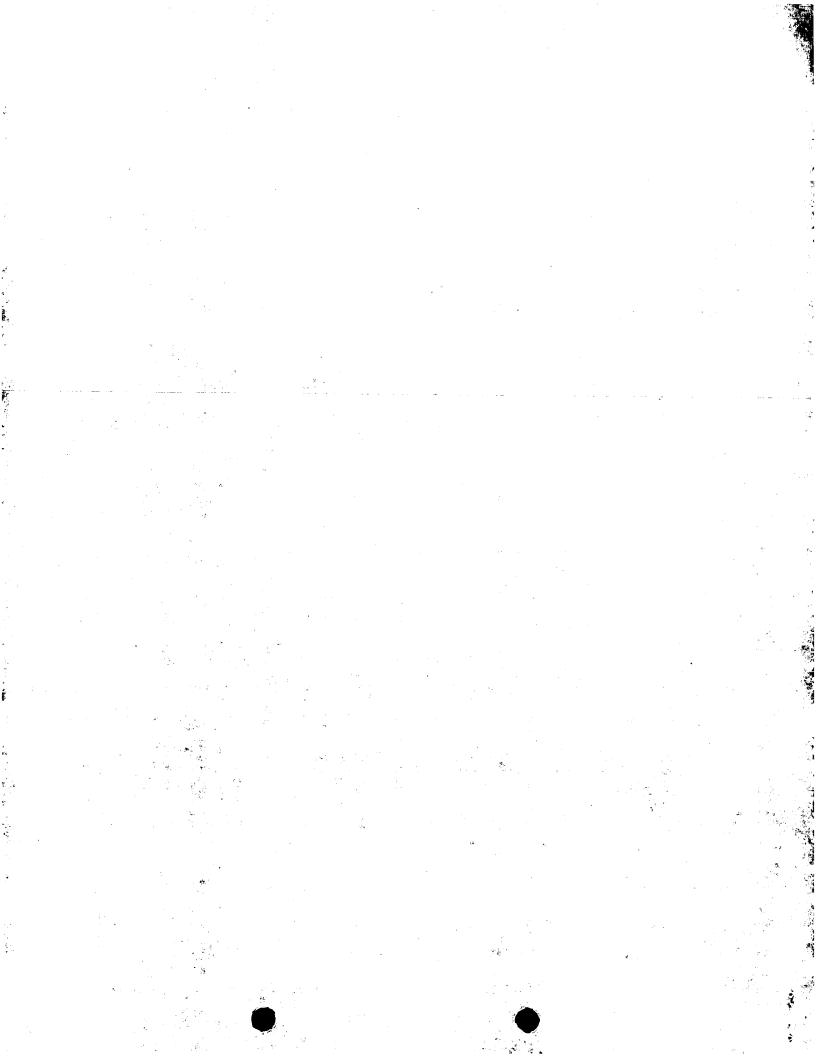
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                                                                                                                                                                                                                     DOMAIN: THE CYTOPLASMIC DOMAIN MAY BE INVOLVED IN THE REGULATION OF TRAFFICKING AND PROTEOLYTIC PROCESSING. REGULATION OF THE PROTEOLYTIC PROCESSING INVOLVES INITIAL INTRACELLULAR DOMAIN DIMERIZATION (BY SIMILARITY).

DOMAIN: ERBB RECEPTOR BINDING IS ELICITED ENTIRELY BY THE EGF-LIKE DOMAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: EXTENSIVE GLYCOSYLATION PRECEDES THE PROTECLYTIC CLEAVAGE (BY
ALSO FOUND IN THE LIVER AND IN THE THYMUS. NOT DETECTED IN HEART, ADRENAL GLAND, OR TESTIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
Growth factor; EGF-like domain; Immunoglobulin domain; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEUREGUIN-2.
NEUREGUIN-2.
NETRACELLULAR (POTENTIAL).
INTERNAL SIGNAL SEQUENCE (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN.
SER/THR-RICH.
POLY-SER.
POLY-SER.
                                                                                                                                                                                                                                                                                                                                                                                                                 PTM: PROTEOLYTIC CLEAVAGE CLOSE TO THE PLASMA MEMBRANE ON THE EXTERNAL FACE LEADS TO THE RELEASE OF THE SOLUBLE GROWTH FACTOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRO-NEUREGULIN-2, MEMBRANE-BOUND FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
M-LINKED (GLCNAC. ..) (POTENTIAL).
MISSING (IN ISOFORM NRG2-BETA).
                                                                       DEVELOPMENTAL STAGE: IN THE EMBRYO, EXPRESSED IN THE BRAIN OF E11.5 EMBRYOS WHERE IT IS FOUND IN THE TELENCEPHALON, BUT NOT THE HINDBRAIN. NOT FOUND IN THE HEART. IN THE ADULT, FOUND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY).
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
SIMILARITY: BELONGS TO THE NEUREGULIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane; Multigene family; Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLY-THR.
POLY-ALA.
POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, D89995; BAA23344.1; -.
EMBL, D89996; BAA23345.1; -.
EMBL, D89997; BAA23346.1; -.
EMBL: D89998; BAA23347.1; -.
EMBL, AB001576; BAA23348.1; -.
HSSP, Q12784; 1HRE.
InterPro; IPR000561; EGF-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003154; Neuregulin.
Pfam; PF00008; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF02158; Neuregulin; 1.
SMART; SM00181; EGF; 1.
SMART; SM00408; IGC2; 1.
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PLV -> FFF (IN ISOFORM NTAK-ALPHA2-1P).

C -> G (IN ISOFORM NTAK-GAMMA). MISSING (IN ISOFORM NTAK-GAMMA). NGFFGORCLEKLLELRINDDPRO -> VGYTGDRCOQFAMV NFS (IN ISOFORM NRG2-BETA). NGFFGQRCLEKLPLRLYMPDPRQKHLGFELKE -> VGYTG DRCQOPAMVNFSK (IN ISOFORM NTAK-BETA). MISSING (IN ISOFORM NTAK-ALPHAZA AND ISOFORM NTAK-ALPHAZB). SSSOWSTYSFTLDLN (IN ISOFORM NRG2-ALPHA). MISSING (IN ISOFORM NRG2-ALPHA). MISSING (IN ISOFORM NRG2-ALPHA). SSSOWSTYSFTLDLN (IN ISOFORM NRG2-ALPHA). SSSOWSTYSFTLDLN (IN ISOFORM NRG2-ALPHA). SSSOWSTYSFTLDLN (IN ISOFORM NRG2-ALPHA). SSSOWSTYSFTLDLN (IN ISOFORM NRG2-ALPHA).	1.1   1.2   1.3   1.4   1.4   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.2   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3   1.3
388 868 412 421 421 439 868 111 724 93776 MW;	3.4%; 19.1%; 19.1%; 19.1%; 20.1%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.2%; 20.
388 389 390 390 414 414 440 117 724 868 AA;	tch  3.4%; 92, Conservative RPDSPRERTPKGKPHAQOP
VARSPLIC VARSPLIC VARSPLIC VARSPLIC VARSPLIC CONFLICT CONFLICT SEQUENCE	Ouery Match Best Local Sin Matches 92; 31 RPDSFP 1   1 :   72QKI 72QKI 134 KSVQDC 123 HRALDJ 185 179 STDSLE 239 PNQGFP 240 SQTGEV 292LQKE 292LQK 293 PNQGFP 339 LNNSKLQR 331 -LNNSKLQR 344 ELY 444 R 448 458 R 458
FT F	Mat

Search completed: February 15, 2003, 08:27:19 Job time : 16.2459 secs



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February 15, 2003, 04:37:08; Search time 33.3512 Seconds (without alignments) 3700.688 Million cell updates/sec
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3199
1 MGAMAYPLLLCLLLAQLGLG.......YMTAVGMWSLVSYDGLTIFQ 599
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GenCore version 5.1.3 copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                  OM protein - protein search, using sw model
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sp_plant:*
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                    imum DB seq length: 0
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                                                                                                                                                                                                                                                                                                                                                                         Title:
Perfect score:
Sequence:
                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                                                                                                   Searched:
                                                                          Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp\_rvirus:\*
sp\_bacteriap:\*
sp\_archeap:\*

#### SUMMARIES

Description	Q9vr40 drosophila	Q9w1p4 drosophila	045500 caenorhabdi	Q9vka3 drosophila	Q9bml5 drosophila	073636 fugu rubrip	Q8sss5 dictyosteli	Q9vps7 drosophila	Q9z0r8 rattus norv	Q9pwel ictalurus p	096954 qeodia cydo	Q9qys2 mus musculu	09v4u3 drosophila	Q9n4t8 caenorhabdi	O8tbh9 homo sapien	
ΠD	Q9VR40	Q9W1P4	045500	Q9VKA3	Q9BML5	1 073636	088885	Q9VPS7	. Q9Z0R8	09PWE1	096954	Q9QYS2	090403	Q9N4T8	08твн9	Q9W1P3
DB	2	Ŋ	2	S	ഗ	13	S	2	11	13	Ŋ	11	Ŋ	Ŋ	4	Ŋ
å Query Match Length DB	699	176	594	1677	1305	868	783	1305	840	977	528	879	738	870	877	264
& Query Match	10.6	7.5	5.7	4.7	4.2	4.1	4.1	4.1	4.0	3.9	3.9	3.8	3.8	3.8	3.7	3.7
Score	339	238.5	181.5	149	134.5	132.5	130.5	130	127.5	125	124.5	120.5	120	120	119.5	117
Result No.	-	7	က	4	Ω	9	7	80	6	10	11	12	13	14	15	16

Q9epv6 mus musculu	073635 fugu rubrip	Q90w16 sparus aura	Q9psyl carassius a	093558 carassius a	Q23587 caenorhabdi	Q9y1a5 lymnaea sta	9		Q9pw88 carassius a	Q63725 rattus norv	O70534 rattus norv	093553 carassius a	Q9y5y9 homo sapien	Q99pg5 mus musculu	093556 carassius a	Q9pwq0 fugu rubrip	6	Q9nyq7 homo sapien	0	O35269 rattus norv	099pg6 musculu	Q925i5 mus musculu	Q923j9 mus musculu	Q8wpn0 oikopleura	Q9vr08 drosophila	Q8r3n3 mus musculu	Q8tdj8 homo sapien	073637 fugu rubrip
Q9EPV6	073635	O90WL6	Q9PSY1	093558	023587	09Y1A5	Q8UZ19	Q8VC98	Q9PW88	063725	070534	093553	Q9Y5Y9	Q99PG5	093556	09PWQ0	062779	Q9NYQ7	Q8RW30	035269	099PG6	092515	0923J9	ONAM80	Q9VR08	Q8R3N3	Q8TDJ8	073637
11	13	13	13	13	S	Ŋ	12	11	13	11	11		4	11	13	13	11	4	10	11	11	11	11	വ	Ŋ	11	4	13
1199	940	940	362	408	3507	540	3105	588	877	2437	383	848	1956	842	350	551	383	3312	955	779	842	842	842	1519	3680	473	457	864
3.6	3.5	3.5	3.5	3.5	3.5	3.4	3.4	3.4	3.4	3.4	3.3	3.3	3.3	3.3	3.3	3.3	3.3	3.3	3.2	3.2	3.2	3.2	3.2	3.2	3.2	3.2	3.2	3.2
115	113.5	112	111.5	111.5	110.5	110	108.5	107.5	107.5	107.5	107	107	107	106.5	106	106	105	104.5	103	102.5	102.5	102.5	102.5	102.5	102.5	102	101.5	101.5
17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

RESULT 1	Q9VR4O PRELIMINARY; PRT; 669 AA. Q9VR4O;	01-MAY-2000 (TrEMBLrel. 01-MAY-2000 (TrEMBLrel.	01-JUN-2001 (TrEMBLrel. 17,	CG11923 protein. CG11923.	Drosophila	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		NCBI_TaxID=7227;	A M MORE SOUTH					George K.A., Lewis S.E., Kichards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,			Abril J.F., Agbayani A., An HJ., Andrews-Ptannkoch C., Baldwin D., Ballow P. M., Bach A., Bayendalo I., Bayraktarodin I., Boselom D.M.		Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier		Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,		Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann	Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,	Glodek		Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketc	Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai 2.,
RE 09	A D	답답	DŢ	G CE	os	8 5	88	OX	2 2	RC	RX	RA	R.	RA RA	RA	RA	KA PA	RA	RA	RA	RA	RA	RA	RA	RA	R A	RA	ΚA

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Query Match
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045500
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                                                                                                                                                                                                                                                                                                                                                                                       22;
Liu X., Mattei B., McIntosh T.C., McLeod M.P., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Am McKulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Nang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Mulliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A G.J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
A Cheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Smith H.O.,
The genome sequence of Drosophila melanogaster.";
EMBL: AE003575; AAF50967.1:
PIyBase: PEGNO031642: CG11923.
InterProf. DROSODM37; GPCR_Mgr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 HNKAYLGSYWRE------LGAAWNSTDGTQ-----EWGAPFRDCNLLTRRWL 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             298 ASGMWTVLETILLGIVLLYASVAVHFFPASTERCLLEPWLRELGFITCYGAIILKLYRHL 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            508 KVFLSRTAQRIPYMTGGRVMRMLAVILLVVFWFLIGWTSSVCQNLEK-QISLIGQGKTSD 566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 GKWPALASAHPSLHRALDTLTHATNFLNVMLQSNKSREQNLQDDLDWYQALVWSLLEGEP 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 SISRAAITFSTDSLSAPAPQVFLQATREESRILLLQDLSSSAPHLA-----NATLETEWF 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 HG---LRRKWRPHLHRRGPNQGPRGLGHSWRRKDGLGGDKSHFKWSPPYLECENGSYKPG 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          281 WLVTLSSAIYGLQPNLVPEFRGVMKVDINLQKVDIDQCSSDGW---FSGTHKCHLNNSEC 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   338 MPIKGL-GFVLGAYECICKAGFYHPGVLPVNNFRRRGPDQHISGSTKDVSE--EAYVCLP 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 LLTENKPAATRDVYTCLCRESYYLPN-STLQGFR------GDRVELSEGYDNYSCIP 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           395 CREGCPFCADDSPC--FVQE----DKYLRLAIISFQGLCMLLDFVSMLVVYHFRKAKSI 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RASGLILLETILFGSLLLYFPVVILYFEPSTFRCILLRWARLLGFATVYGTVTLKLHRVL 507
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48 --TRAEVSRRANGIAS-----YALNEDDNLLAFAIAAPSIHTVVVKFRDNVTIPPDQV 98
                                                                                                                                                                                                                                                                                                                                                                                                                                             6 GKWPC-RMFYDYTDIAEDAARQFIEFL----SGKFPNANTPIAID-------EP 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98;
                                                                                                                                                                                                                                                                                                                                                         Length 669;
                                                                                                                                                                                                                                                                                                                                                       10.6%; Score 339; DB 5; Length 66 25.6%; Pred. No. 1.2e-20; ive 71; Mismatches 200; Indels
                                                                                                                                                                                                                                                                                                               G_PROTEIN_RECEP_F3_4; 1.
; 75242 MW; FFE5721445DAB5F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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                                                                                                                                                                                                                                                                                                                                                                                      Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    567 HLIFNMCLIDRWDYMT 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----NTCHPLKWELVT 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                Pfam; PF00003; 7tm_3; 1. PROSITE; PS50259; G_PRO1
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                            669 AA;
                                                                                                                                                                                                                                                                                                                              SEQUENCE
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Q9W1P4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    448
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RECORDING—20196005; PubbMed=10731132;

REDAINNE—20196005; PubbMed=10731132;

RADAMAREKELEY.

RADAGINE—20196005; PubbMed=10731132;

RADAGINE—20196005; S.Chorer S.E., Lip P.W., Hoskins R.A., Galle R.F.,

RADAGINE—20196005; S.Chorer S.E., Lip P.W., Hoskins R.A., Galle R.F.,

RADAGINE M.D., Celniker S.E., Richards S., Ashburner M., Ffeliffer B.D.,

RADADIL J.F., Doyle C., Baxeer E.G., Helf G., Nelson C.R., Miklos G.L.G.,

RADADIL J.F., Doyle C., Baxeer E.G., Helf G., Nelson C.R., Miklos G.L.G.,

RADADIL J.F., Doyle C., Baxeer E.G., Helf G., Nelson C.R., Miklos G.L.G.,

RADADIL J.F., Doyle C., Baxeer E.G., Helf G., Nelson C.R., Miklos G.L.G.,

RADADIL J.F., Doyle C., Baxeer E.G., Helf G., Nelson C.R., Miklos G.L.G.,

RADOROVA D., Bocchan M.R., Bouck J., Brokstein D., Berotlier P.,

RADOROVA D., Bocchan M.R., Bouck J., Brokstein D., Berotlier P.,

RADOROVA D., Bocchan M.R., Bouck J., Brokstein D., Davids P.,

RADOROVA D., Bocchan D.A., Butller H., Cadleu E., Center A., Chandra I.,

RADOROVA D., Bocchan M.R., Bouck J., Brokstein P., Brottisr P.,

RADOROVA D., Bocchan D.A., Butller H., Gadleu E., Davies P.,

RADOROVA D., Bocchar A., Deng Z., Mays A.D., Dav I.D. Diez S.M.,

RADOROVA D., Bocchar A., Deng Z., Mays A.D., Dav I.D. Diez S.M.,

RADOROVA D., Houston K.A., Howland T.J., Weil M.H., Index M.R.,

RADOROVA M., Hursey D., Heiman T.J., Hernandez J.R., Houck J.,

RADIALIS E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RADIALIS E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RADOROVA M., Mulshina G.H., Misskenn D.R., Packleb J.M.,

RADOROVA M., Mulshina M., Mondary C., Morris J., Moshreff A.,

RADOROVA M., Mulshina M., Shan S., Pollard J., Pull M., Nelson D.L.,

RADOROVA M., Mulshina M., Strong R., Santh T.,

RADOROVA M., Manghor M., Strong R., Santh T.,

RADOROVA M., Shong F.N., Zabon M., Strong R., Santh T.,

RADOROVA M., Manghor M., Weinselber D., Wang S., Zhu X., Smith H.O.,

RADOROVA M., Shong F.N., Santh M., Strong S., Zhu X., Smith H.O.,

RADOROVA M., Manghor M., Weinselder S., Calebatter T.,

                       Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              352 CICKAGFYHPGVLPVNNFRRRGPDQHISGSTKDV------SEEAYVCLPCRE 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLCRKGFYFPDIVSQHKF----FNGSLLEEEYEKLMLGKNSTYNSNSEYECLPCAE 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19661 MW; 524E4E2C48CB7D33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.5%; Score 238.5; DB 5; 31.5%; Pred. No. 1e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 594
Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                       STRAIN-BERKELEY;
                                                                                                                                           NCBI_TaxID=7227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52;
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MEDLINE=20196006; PubMed=10731132;
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les 58; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           320 SDGW---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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      g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           259 DKSHFKWSPPY------LECENGSYKPGWLVTLSSAIYGLQPNLVPEFRGVM 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104 DKSSFQQIPPFDVSFARRTHFYGLQLNCTGNNHR--WLPRL--VFVSHDPN---NSNKKA 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        157 YLTLQLDQFDVDMCS-------AVNCHTKCTWTVHGGL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 424 QGLCMLLDFVSMLVVYHFRKAKSIRASGLILLETILFGSLLLYFPVVILYFEPSTFRCIL 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        218 NSICALI-CIALIPIVCYQRKRQHEARGWALMELFLIGASILYSVLFLDFVAPPEYGCCV 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WT-----SSVCQNLEKQISLIGQGKTSDHLIF-----NMCLIDRWDYMTA 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      336 WIVGSWGDTALWRTAWPQCLMQGWHVIWHGYELLFLLYAVRLCYKARNSDWLERWQFTVA 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | :||: ||: ||: ||: ||: || ||: || ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      365 PVNNFRRRGPDQHISGSTKDVSEEAYVCLPCREGCPFCADDSPCFVQED-KYLRLAIISF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    484 LRWARLLGFATVYGTVTLKLHRVLKVFLSRTAQRIPYMTGGRVMRMLAVILLVVFWFLIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RVS-----CNSDDVILCRTDAERGRHMLLAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 103;
                                                                                                                                                                                                                                                                                                                                                                                   Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                 Dobson R.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           80AF1FC165AB9070 CRC64;
                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.7%; Score 181.5; DB 5; 19.6%; Pred. No. 4.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1677 AA
                                                                                                                                                           Rhabditidae; Peloderinae; Caenorhabditis
NCBI_TaxID=6239;
      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
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                                                                                                                                                                                                                                                                                                                                         MEDLINE-99069613; Pubmed-9851916;
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                                                                                                                                                                                                                                                                                                                                                                                                     investigating biology.";
Science 282:2012-2018(1998).
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 19.6
Matches 72; Conservative
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01-JUN-1998 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.
                                                                                                               Caenorhabditis elegans.
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              396 VCLEAVIT 403
                                                                     F39B2.8 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z928
SEQUENCE
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Adding M.D., Celoliker S.E., Holf R.A., Evans C.A., Gocayne J.D., R.A. Adding M.D., Celoliker S.E., Holf R.A., Evans C.A., Gocayne J.D., R.A. Adding M.D., Celoliker S.E., Holf R.A., Evans C.A., Gocayne J.D., R.A. George R.A., Lewis S.E., Richards S.., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Bardon R.C., Rogers Y.-H.C., Blazej K.G., Champe M., Pfelifer B.D., R.A. Mandon R.A., Bardon R.C., Baldwin D., Ballew R.M., Basu A., Barendale J., Bayraktaroglu L., Basaley E.M., Ballew R.M., Basu A., Barendale J., Bayraktaroglu L., Basaley E.M., Ballew R.M., Botcham M.R., Bouck J., Bayraktaroglu L., Basaley E.M., Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., RA Grerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., R.A. Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., M. Cawley S., Dahlke C., Davenport L.B., Davies P., Botcham M.B., Bouck J., Bayraktaroglu L., Betasch M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., R.A. Gong F., Gorrell J.H., Gu Z., Gunn P., Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Harris M.A., Gong F., Gorrell J.H., Gu Z., Genbart W.M., Glasser K., Alballi M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeeyam C., Lasko P., Lei Y., Levitsky A.A., Li J., Ji Z., Liang Y., Lin X., Mirmel B.E., Kodira C.D., Kraft C., Morris J., Moshrefi A., Mount S.M. Moy M., Murphy B., Murphy L., Mazay D.M., Nelson D.L., Merkulov G., Milshina N.V., Mobarry C., Morris J., Woshrefi A., Mount S.M., Mount S.M., Nalos B., Suben H., Shier E., Spradling A.C., Stapleton M., Stupski M.P., Smith H.O., Alliams S.M., Wodser T., Wolly K., Walssehbach J., Maying Z.-Y., Wassarman D.A., Walssehbach J., Wallshiman S.M., Wodser J.C., Schoeler E., Wassarman D.A., Walshillow M., Shuge S.C., Shen H., Spier E., Spradling A.C., Shan M., Shuge S.C., Shan W., Wodser J., Shan S., Pollard Y., Walls S., Paleng X.H., Zhong F.N., Zhong F.N., Zhong F.N., Zho 265 WSPPYLECENGSYKPGWLVTLSSAI-----YGLQPNLVPEFRGVMKVDINLQKVDIDQCS 319 -----FSGTHKCHLNNSE 336 147 AEPYPFGSRRQKMQQLQTHNRLGARRSLFLGSRMGAIDESTINDLQAFHSSHKCH--RTS 204 205 MVPVKRLNRKIKEPVSPKLSANQNVTPTRRIKRINTPVAVDPSPSPSVVARRARTSAALK 264 SFINKYRREHPGKLRAEVVSIWRKMSVEEKQAFQRIGTIQETPTHVHFEEEEVPVPISND 324 -----GFVLGAYECICKAGFYHPGVLPVNNFRR 371 325 VIDIVECDYRQPSAETPTVTGGKLLTTLTGSSSWTRGSYQCLCRGGFY----SL 374 4.7%; Score 149; DB 5; Length 1677; 14.3%; Pred. No. 0.0014; ive 37; Mismatches 83; Indels 228 PROSITE; PS00133; CARBOXYPEPT\_ZN\_2; UNKNOWN\_1.
PROSITE; PS50259; G\_PROTEIN\_RECEP\_F3\_4; 1.
SEQUENCE 1677 AA; 188028 MW; F50A8D282A8E3B6E CRC64; EMBL; AE003635; AAF53175.1;
FlyBases; FR980032448, CG17215.
InterPro; IPR000524; Cation\_efflux.
InterPro; IPR000837; GPCR\_Mgr.
InterPro; IPR000834, Zn\_carbopept.
Pfam; PP01545; Cation\_efflux; 1.
TIGREAMS; TIGR01297; CDF: 1. Conservative

8

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279 HSRIKRVADVIRRSTAVVVVAFTASTEMMILLEELSHEPSPPROWIGSESWVT---DPDL 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            232 PHLHRRGPNQGPRGLGHSWRRKDGLGGDKSHFKWSPPY....-LECENGSYRPGWLV--- 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 HPSLHRALDTLTHATNFLNVMLQSNKSREQNLQD------DLDWYQALVWSLLEGEPSI 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172 SRAAITFSTDSLSAPAPQVFLQATREESRILLQDLSSSAPHLANATLETEWFHGLRRKWR 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----TLSSAIYGLQPNLVPEFRGVMKVDINLQKVDIDQCSSDGWFSGTHKCH 331
                                                                                                                                                                                                                                                                                                                                                                                                           Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
NCBI_TaxID=31033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Putative pheromone receptors related to the Ca2+-sensing receptor
LR--FSFCAGTIGFAIQRSVIPGLRD----FLLDLSPS--KVASSPVLTEF-----WE
                                                                 WARLL--GFATVYGTVTLKLHRVLKVFLSRTAQ------RIPYMTGGRVMRMLAVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DSFNCR------LGKGERMCD---GSEDIMTLQSPYTDTSELRITNMVYKAVYAIAHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-98226788; PubMed=9560249;
Naito T., Saito Y., Tamamoto J., Nozaki Y., Tomura K., Hazama M., Nakanishi S., Brenner S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 13; Length 868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95531 MW; 3FC66EB1E9972E01 CRC64;
                                              433 VSMLVVYHFRKAKSIRASGLILLETILFGSLLLYFPVVILYFEPST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 95:5178-5181(1998).

EMBL, AB008858; BAA26123.1; -.
InterPro; IPR001828; ANF_receptor.
InterPro; IPR001838; GPCR_Mgr.
InterPro; IPR002052; NG_Mtase.
InterPro; IPR04073; Vmron_receptor2.
Pfam; PF001094; ANF_receptor; IPP011994; ANF_receptor; IPPN0185; VOMFRONASIZR.
PRINTS; PR01248; GPCRMGR.
PRINTS; PR01535; VOMFRONASIZR.
                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 07, Last sequence update) (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.1%; Score 132.5; DE 19.7%; Pred. No. 0.015;
                                                                                                                                                                                                                                                                                               AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74; Mismatches
                                                                                                                                                                                                                                                                                               868
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                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                              LLVVFWFLIGWTSSVCQNLEKQIS 557
                                                                                                                                                                                                   07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 113; Conservative
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01-MAR-2002
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                                                                              640
                                                                                                                486
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             420
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                                              434
                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pteryyota; Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LASAHPSLHRALDTL----TH-----ATNFLNVMLQSNKSREQNLQDDLDWYQALVW 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --FHGQDGFG-----SGYGPRISIAATQSDSRRRRRGVVGTSGGHLFPEAISO 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RSTDGTILAQKLAEEVPMDVASYLYTGDSHQLKRANCSGR-----YELAGLPGKWP--A 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RETDTRIIIGSFSQELAPQILCEAY-----RLRMFGADYAWILHESMGAPW-WPDQR 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          536 FLQQMGKLHFLGVSGPVSFSGPDRVG----TTAFYQIQ-----RGL----LEPVA 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        373 GPDQHISGSTKDVSEEAYVCLPCREGCPFCADDSPCFVQEDKYLRLAIISFQGLCMLLDF 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
             -QHISGSTKDVSEEAYVCLPCREGCPFCADDSPCFVQEDKYLRLAI
                                            375 RHPDGFNGTIMEIAWQEQQDNISNYYSEVFKCLPCAPGCDTCTGPEPCLANYHWPFRISL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YLE--------CENGSYKPGWLVTLSSAIYGLQPNLVPEFRGVMKVDINLQKVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         315 IDQCSSDGWFSGTHKCHLNNSECMPIKGLGFVLGAYECICKAGFYHPGVLPVNN--FRRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               395 TACSNHELQLAVENLIVVSTHNSIVGNNVSYSGLNNHMFNSQLRKQSAQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLLEGEPSISRAAITFSTDSLSAPAPQVFLQATREESR------ILLQDLSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SAPHLANATLETEWFHGLRRKWRPHLHRRGPNQGPRGLGHSWRRKDGLGGDKSHFKWSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YAPQ----TYDAVWAIALALRAAEEHWRRNEEQS------KLDGFDYTRSDMAWE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1305;
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-21097320; PubMed-11168554;
Mezler M., Muller T., Raming K.;
"Cloning and functional expression of GABA-B receptors from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8BBFA80F0E9BEADD CRC64;
                                                                                                             435 LTISIGCACGTFVLAGYLFRHRRVKVFKVASPIFLMITLIGCAIMY
                                                                            421 ISFQGLCMLLDFVSMLVVYHFRKAKSIRASGLILLETILFGSLLLY
                                                                                                                                                                                                                         01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2002 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative metabotropic GABA-B receptor subtype 3.
GABA-B-R3 OR CG3022.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, AF318274; AARI3422.1;
EMBL, AF318274; AARI3422.1;
ELYBase; FEB1001375; GABA-B-R3.
InterPro; IPR001838; ANF_receptor.
InterPro; IPR000037; GPCR_MGr.
Pfam; PF001094; ANF_receptor; 1.
PRINTS; PR00248; ANF_receptor; 1.
PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.2%; Score 134.5; DB 5;
18.8%; Pred. No. 0.017;
tive 80; Mismatches 179;
                                                                                                                                                                                             PRT; 1305 AA
                                                                                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eur. J. Neurosci. 13:477-486(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1305 AA; 143701 MW;
                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
             372 RGPD-----
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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SEQUENCE
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RA Adams M.D. Celniker S.E., Lip. R., Evans C.A., Gocayne J.D.,
RA Adams M.D. Celniker S.E., Lip. R., Fivens C.A., Gocayne J.D.,
RA Adams M.D. Celniker S.E., Lip. R., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Lip. R.A., Foshins R.A., Galle R.F.,
RA Barandides C.G., Rogers Y.-H.C., Blazej R.G., Champpe M., Pfelifer B.D.,
RA Barlu J.F., Apdayani A., An H.-J., Andrews-Pennicoh C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Barendale J., Bayraktaroglu L., Badsley E.M.,
Ballew R.M., Basu A., Barendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Barendale J., Bayraktaroglu L., Beasley E.M.,
Ballew R.M., Cawley B., Buttler H., Caddeu E., Center A., Chadra I.,
RA Burtis R.C., Busam D.A., Buttler H., Caddeu E., Center A., Chadra I.,
RA Burtis R.C., Busam D.A., Buttler H., Caddeu E., Center A., Chadra I.,
RA Cadory S., Dahlke C., Davenport L.B., Davies P.,
RA Cheffer J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Codors B., Delcher A., Domes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Burtis R.C., Gabriellan A.E., Garg M.S., Gelbart W.M., Glasser K.,
RA Goong F., Gorrell J.H., Gu Z., Gunn P., Harris M.L., Harvey D., Heimman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Liu X., Mattei B., McThtosh T.C., Moshrefl A.,
RA Nelson D.R., Najon K.A., Li J., Li Z., Liang Y., Lin X.,
Ralush R.A., Remington K.A., Muson R., Porlard J., Moshrefl A.,
Ralus R.A., Remington R., Saunders R.D.C., Scheeler F., Shen H.,
Ray Spier E., Spradling A.C., Stangeron D., Worles D., Wang X.,
Ray Ster E., Spradling A.C., Stangeron M., Strong R., Wassarman D.A., Weinstook M., Wang X.,
Ray Wallsh R.A., Woorlage T., Worley R. Sung S., Pall Y., Wang X.,
Ray Ster E., Spradling A.C., Stangeron M., Strong R., Wallsenber M.,
Ray Lang S.H., Woodage T., Worley K.C., Wu D., Yang S., Zhon G., Stene C. BR., Weissenber M.,
R. Science 287:2185-2195(2000)
R. Science 287:2185-2195(200)
R. Bublis R.D. Stone R.D. Wooley C., Wu D., Yang S., Zhon M., Science 287:2185-2195(200)
R. B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 HLHRRGPNQGPRGLGHSW-------RRKDGLGGDKSHFKWSPPYLECENGSY 277
                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 130; DB 5; Length 1305; Pred. No. 0.043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00248; GPCRMGR.
PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
PROSITE; PS00041; HTH_ARAC_EMILY_1; UNKNOWN_1.
SEQUENCE 1305 AA; 143588 MW; A9C3C85307650450 CRC64;
                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4.1%; Score 130; 19.2%; Pred. No. 0
                                                                                                                                                                                                                                                                     STRAIN=BERKELEY;
MEDLINE=20196006; Pubmed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FlyBase; FBgn0031275; GABA-B-R3.
InterPro; IPR001828; ANF_receptor.
InterPro; IPR000337; GPCR_Mgr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000005; HTHArac.
Pfam; PF00003; 7tm_3; 1.
Pfam; PF01094; ANF_receptor; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68;
(TrEMBLrel. 13, TrEMBLrel. 16, (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87; Conservative
                                                                                       GABA-B-R3 OR CG3022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sest Local Similarity
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                   NCBI_TaxID=7227;
                                       01-JUN-2001
CG3022 prote
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tungal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.; Sequence and Analysis of Chromosome 2 of Dictyostelium."; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; AC116032; AAL93018.1; SEQUENCE 783 AA: 87581 MW; 91F1EC8FB92390D7 CRC64;
                                                                                                            405
                                                                                                                                                                                                                                                                                                                                      701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    469 VVILYFEPSTFRCILLRWARLLGFATVYGTVTLKLHRVLKVF----LSRTA----QRIPY 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                521 MTGGRVMRMLAV-ILLVVFWFLIGWTSSVCQNLEKQISLIGQGKTSDHLIFNMCLIDRWD 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            584
                                                                                                                                                                                                     454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           409 FVQEDKYLRLAIISFQGLCMLLDFVSMLVVYHFRKAKSIRASGLILLETILFGSLLLYFP 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :: |: | : | : | : | : 432 CILFAQSPINQTCSARIWILSLGYTUFLGNILVKNWRIWILFDNPKLKKRAITNWKLYPW 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                    525 GRKQVPVSVCSDSCPQGTRKVLQKGKPICCYDCVQCPEGEISNVTDSPECIPCLDDFWPN
                                                                                                                                                                                                                        ---SPCFVQEDKYLR-----LAIISFQGLCMLLDFVSMLVVYHFRKAKSIRASGLIL
                                                                                                                                                                                                                                                                                       455 LETILFGSLLLYFPVVILYFEPSTFRCILLRWARLLGFATVYGTVTLKLHRVLKVFLSRT
                                                                                                                                                                                                                                                                                                                                  SFLLLFSLTLCFLCSLTFIGAPSHLSCMLRHTAFGITFVLCISCVLGKTVVVLMAFRAT-
                                                                                                                                                                                                                                                                                                                                                                                 ---RMLAV-----ILLVVFWFLIGWTSSVCQNLEKQISLIG
                                                                                                                                                                                                                                                                                                                                                                                                           --NGYAVSFDANGDPVASYELVNWKKSGSGSIEVVPVGYYDASLPEGQEFRIFRDITWVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 783;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
METABOTROPIC GABA-B receptor subtype 2. 6/101.
Dictyostellum discoideum (Slime mold).
Eukaryota: Mycetozoa: Dictyostellida; Dictyostellum.
NBI_TAXID=44689;
                                                                                                            -RRRGPDQHISGS----TKDVSEE----AYVCLPCREG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 5;
                     LNNSECMPIKGLGFVLGAYECI - - CKAGFYHPGVLPÝNNF -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.1%; Score 130.5; DB
21.7%; Pred. No. 0.019;
Live 44; Mismatches E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     561 QGKTSDHLIFNMCLIDRWDYMTAVGMWSLVSYDGL 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --TTYKERIILECALG-----SSVGFWAVLGYIGL 774
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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443 QFH-----GQDGFGSGYGSRISIAATQSDSRRRRRRGVGGTSGGHLFPEAISQYAPQTY
                                                                                          278 KPGWLVTLSSAIYGLQPNLVPEFRGVMKVDINLQKVDIDQCSSDGWFSGTHKCHLNNSEC
                                                                                                                                                          -----RAAEEHW------RRNEEQ
                                                                                                                                                                                                                       MPIKGLGFVLG--AYECICKAGFYH-PGVLPVNNFRRRGPDQHISGST-----KDVSEE
                                                                                                                                                                                                                                                                --FRCILLRWARLL--GFATVYGTVTLKLHRVLKVFLSRTAQ-------RIPYMTGG
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Hoon M.A., Adler E., Lindemeier J., Battey J.F., Ryba N.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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Last annotation update)
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Cell 96:541-551(1999).
EMBL; AF127389; AAD18069.1; -.
InterPro; IPR001828; ANF_receptor.
InterPro; IPR000337; GPCR_Mgr.
Pfam; PF00003; 7 fm_3; 1.
Pfam; PF001094; ANF_receptor; 1.
PRINTS; PR00248; GPCRMGR.
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01-MAY-1999 (TrEMBLrel. 10, Last sequenc
01-JUN-2002 (TrEMBLrel. 21, Last annotat
Putative taste receptor TR1 (Fragment).
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Hellmich H.L., Micci A.M., Sanchez X., Christensen B.N.;
Hellmich H.L., Micci A.M., Sanchez X., Christensen B.N.;

"Molecular cloning, functional expression and localization of a novel metabortropic glutamate receptor linked to calcium mobilization from the catfish retina.";

L. Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.

EMBL, AFOTÓ473; AAD47893.1;

R. InterPro; IPR001828; ANF_receptor.

R. InterPro; IPR001828; ANF_receptor.

R. PRONO03; 7fm_3; 1.

R. PRONO03; 7fm_3; 1.

R. PRONO09; G-PROTEIN_RECEP_F3_1; 1.

R. PROSITE; PS00981; G-PROTEIN_RECEP_F3_3; 1.

R. PROSITE; PS0029; G-PROTEIN_RECEP_F3_4; 1.
                                                                                                                                           616 CSFY----SFEGEPTVPACLLRQPLFSLGFAIFLSCLTIRSFQLVIIFKFSTKVPTFYRT 671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         572 CEPCDGYQYQVGELTCEMCPFDMRPTANHTACTPTFIIKLDWHSPWAVVPMFLAILGIAA 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
Ictaluridae; Ictalurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | : | : | : | | GMCITYSAMLTKTNRIYRIFEQGKKSVTAPKFISPTSQLVITFILVSFQVIGVFIWF 748
EFLAWHEPISLVLIAANTLLLLLLVGTAGLFAWHFH-TPVVRSAGGRLCFLMLGSLVAGS
                                                                                                  463 LLLYFPVVILYFEPSTFRCILLRWARLLGFATVYGTVTLKLHRVLKVFLSRTAQRIPYMT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 491 GFATVYGTVTLKLHRVLKVF----LSRTAQRIPYMTGGRVMRMLAV---ILLVVFWF 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 977;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    108759 MW; BD06A67E240751CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Metabotropic glutamate GABA-like receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Last sequence un 01-JUN-2001 (TrEMBLrel. 17, Last annotation Metabotropic glutamate receptor (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 125;
Pred. No. 0
                                                                                                                                                                                                                                523 -----GGRVMRMLAVILLVVFWFLIGWT 545
                                                                                                                                                                                                                                                                            672 WAQNHGAGLFVIVSSTVHLLICLTWLVMWT 701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ictalurus punctatus (Channel catfish).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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879 AA;
                                              91;
 SEQUENCE
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                                              Matches
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                                                                                                                                                                                                                                                                                          475 EPST----FRCILLRWARLLGFATVYGTVTLKLHRVLKVFLSRTAQRIPYMTGGRVMR 528
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                           415 YLRLAIISFQGLCMLLDFVSMLVVYHFRKAKSIRASGLILLETILFGSLLLYFPVVILYF 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                            Perovic S., Krasko A., Prokic I., Mueller I.M., Mueller W.B.G.;
"Origin of neuronal-like receptors in Metazoa: cloning of a metabotropic glutamate/GABA-like receptor from the marine sponge Geodia cydonium.";
Cell Tissue Res. 296:395-404(1999).
BMBL; WIZ11; CAA76688.1;
InterPro; IPRO0033; 7tm.3; 1.
PROSITE; PS50259; G_PROTEIN_RECEP_F3_4; 1.
                                                                                                                                                                                                                                                      15;
           Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
Astrophorida; Geodiidae; Geodia.
                                                                                                                                                                                                                              Length 528;
                                                                                                                                                                                                                           3.9%; Score 124.5; DB 5; Length
32.6%; Pred. No. 0.036;
Live 20; Mismatches 52; Indels
                                                                                                                                                                                                     528 AA; 58641 MW; 0B99D8357FEAB3B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              879 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1. PROSITE; PS00980; G_PROTEIN_RECEP_F3_2; 1. PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1. PROSITE; PSS0259; G_PROTEIN_RECEP_F3_4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Metabotropic glutamate receptor 3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Blochem. 126:889-896(1999).

BMBL: AR170601: AAR06741.1;

EMBL: AR170698; AAR06741.1;

EMBL: AR170699; AAR06741.1;

EMBL: AR170699; AAR06741.1;

INTERPORT OF AAR06741.1;

INTERPORT OF AAR06741.1;

INTERPORT OF AR06741.1;

Fâml: PRO01094;

PRINTS;

PRINTS;

PRO0248;

GPCRMGR.
                                                                     MEDLINE-99311290; PubMed-10382281;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-20012997; PubMed=10544282;
                                                                                                                                                                                                                                                   42; Conservative
 cydonium (Sponge)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
                                                                                                                                                                                                                                        Local Similarity
                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                 252 DYALALFWY 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                            529 MLAVILLVV 537
                                   NCBI_TaxID=6047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=129/SV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 astrocytes.";
                                                                                                                                                                                            Receptor.
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                                                                                                                                                                                                      SEQUENCE
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Babril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Beason K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchien M.R., Bouck J., Brokstein P., Brottier P., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
                                                                                                                                                                                                                                                                                                                                                                                    189 QVFLQATREESRILLQDLSSSAPHLANATLETEWFHGLRRKWRPHLHRRGPNQGPRGLGH 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 SWRRK--DGLGGDKSHFKWSPPYLECENGSYKP-----GWLVTLSSAIYGLQPNLVP 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -WEOKFOCSLONKRNHROICDKHLAIDSSNYEQESKIMFVVNAVYAMAHALHKMORTLCP 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---NTTKLCDAMKILDGKKLYKDYLLKINFTAPFN-----PNKGA------DSIVKFDT 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             575 AWAIGPVIIACLGFMCTCIVI----TVFIKHNNTPLVKASGRELCYILLFGVSLSYCMT 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 VMLQSNKSRE----QNLQDDLDWYQALVW----SLLEGEPSISRAAITFSTDSLSAPAP 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             459 YGDGMGRYNVFN----FQHIGGKYSYLKVGHWAETLYLDVDSIHWSRNSVPTSQCSDPCA 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----ADDSPCFVQEDKYLR----417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     515 PNEMKNMOPGDVCCWICIPCEPYEYLVDEFTCMDCGPGQWPTADLSGCYNLPEDYIRWED 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             299 EFRGVMKVDINLQKVDIDQCSSDGWFSGTHKCHLNNSECMPIKGLGFVLGAYECICKAGF
                                                                                                                                                                                                                                                                                                        274 LFMRSDDSRELIAAASRVNASFTWVASDGWGAQESIVKGSEHVAYGAITLELAS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----HPVRQFDR-YFQSLNPYNNH-----RNPWFRDF-----
                                                                                                                                                    Indels 159;
                                                                            DB 11; Length
99114 MW; F3A8B26CE96679EF CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                Mismatches 185;
                                                                    3.8%; Score 120.5; DE 18.2%; Pred. No. 0.16;
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STRAIN-BERKELEY;
MEDLINE-20196006; PubMed=10731132;
                                                                                                                                                65;
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                                                                                                                                                        Conservative
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                                                                    Query Match
Best Local Similarity
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467 FPVVILYFEPSTFRCILLRWARLLGFATVYGTVTLKLHRVLKVFLS--RTAQRIPYMTGG 524
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                                                                                                                                                                                                                                                               09N4T8
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Q8TBH9
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RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangelista C.C., Ferrac C., Ferraca S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M.,
RA Hostin D., Houston K.A., Helman T.J., Helmandez J.R., Houck J.,
RA Hastin N.L., Harvey D., Helman T.J., Wal M. H., Ibegwam C.,
RA Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jasko P., Lei Y., Levitsky A.A., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B.E., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Murphy D.M., Nelson D.L.,
RA Palazzolo M., Pittuan G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spler E., Spradling A.C., Stapleron M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinselbech M., Zhong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang S., Yao Q., A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhong S., Zho Q., Zheng L.,
RA Sheng X.H., Zhong P.N., Rubin G.M., Venter J.C.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
R. The genome sequence of Drosophila melanogaster.";
R. Schace 287:1185-2195(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RYNIIHFKQSQA------GQYHWV-KVGEYTEGELRLNMTEVKFKRLSPKPPESV 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EIYLRPESAWAIGAMAFSATGILVTLFVMGVFVRHNDTPIVRASGRELSYILLAGIFMCY 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAQKLAEEVPMDVASYLYTGDS-----HQLKRANCSGRYELAGLPGKWPALASAHPSLH 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RALDTLTHATNFLNVMLQSNKSREQNLQDDLDWYQALVWSLLEGEPSISRAAITFSTDSL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SAPA---PQVFLQATREESRILLQDLSSSAPHLANATLETEWFHGLRRKWRPHLHRRGPN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------DQLQFVSDA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             207 VMAFAYALRDMHRDLCGGGPSLCEAMKPTKGADLLKYLRKVEFEGLSGDEFRFDGNGDGP 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GSTKDVSEEAYVCLPC-----REGCPFC-----ADDSPCFVQE 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DKYLR-----LAIISFQGLCMLLDFVSMLVVYHFRKAKSIRASGLILLETILFGSLLLY 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----DYEPEVEG---TLSVQPQ 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    289 I ---- YGLQ------ PNLVPEFRGVMKVDI--NLQKVDIDQCSSDGW-FSGT--- 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QGPRGLGHSWRRKDGLGGDKSHFKWSPPY - - - - - - - - LECENGSYKPGWLVTLSSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---HKCHLNNSECMPIKGLGFVLGAYECICKAGFYHPGVLPVN----NFRRGPDQHIS-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.8%; Score 120; DB 5; Length 738
18.8%; Pred. No. 0.14;
.ive 63; Mismatches 198; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00003; 7tm_3; 1.
Pfam; PF01094; ANF_receptor; 1.
PROITS; PR00248; GPCRMGR.
PROSITE; PS00981; G_PROTEIN_RECEP_F3_3; 1.
PROSITE; PS50259; G_ROTEIN_RECEP_F3_4; 1.
SEQUENCE 738 AA; 83179 MW; 0E6620337B059EAC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FlyBase; FBgn0033298; CG8692.
InterPro; IPR001828; ANF_receptor.
InterPro; IPR000337; GPCR_Mgr.
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Matches 106; Conserve
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436 GVTFALVLKPTNIVCAIQRFGVGFCFTVVYAALLTKTNRIARIFKAGKQSAKRPSFISPK 495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STIFVVSVFLKFSNTPVIMASGRELCYCMMSGIGMCYTLTFFLVSQPTVITCSMTRILM 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 489 LLGFATVYGTVTLKLHRVLKVFLSRTAQRIPYMTG----GRVMRMLAVILLVVF-WFLIG 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | : :| : | :| : | :| | CLSMSAIYAAIITKINFLARVFKPDSAORPRFITPKAQVGICMGIVSVQLIGTFVWILFD 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.8%; Score 120; DB 5; Length 870; 22.7%; Pred. No. 0.18; Live 35; Mismatches 102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The sequence of C. elegans cosmid Y4C6A.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
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InterPro; IPR001828; ANF receptor.
InterPro; IPR001828; ANF receptor.
InterPro; IPR001837; GPCR_Mgr.
Pfam: PF01094; ANF receptor; 1.
PFINTS; PR00248; GPCRMGR.
PROSITE; PS00259; GPCRMGR.
SEQUENCE 870 AA; 97727 MW; 2FCE2F871D6B1EF9 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                     Created)
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STRAIN-BRISTOL N2;
MEDLINE-99069613; Pubmed-9851916;
                                                                                                                                          496 SQLVICACLVSVQILINGVWMVI 518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Layman D., Graves T., Yoakum M.;
"The sequence of C. elegans cosm:
                                                                                525 RVMRMLAV----ILLVVFWFLI 542
                                                                                                                                                                                                                                                                                                                                                               01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-JUN-2002 (TrEMBLrel. 21, Y4C6A.2 protein.
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Matches 49; Conservative
                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
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23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           527
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                         01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01 dutamate receptor, metabotropic 3.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                          uery Match 3.7%; Score 119.5; DB 4; Length 877; lest Local Similarity 18.8%; Pred. No. 0.2; atches 91; Conservative 71; Mismatches 194; Indels 129;
                                                                                                                                                                                              Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC022496; AAH22496.1;
                                                                                                                                                                                                                                             Receptor.
SEQUENCE 877 AA; 98673 MW; 034E82640341FB24 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   326 ----QPVRQFDR-YFQSLNPYNNH-----RNPWFRDF----
 877 AA
 PRT;
 PRELIMINARY;
                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE-BRAIN;
                                                                                                                                     NCBI_TaxID=9606
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Search completed: February 15, 2003, 08:31:02 Job time : 42.3512 secs



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APPLICATION NUMBER:
FILING DATE: 12 Feb
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US-08-485-588-8
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1524.948 Million cell updates/sec
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/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
/cgn2_6/ptodata/1/laa/6A_COMB.pep:*
/cgn2_6/ptodata/1/laa/6B_COMB.pep:*
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/cgn2_6/ptodata/1/laa/PCTUS_COMB.pep:*
GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
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### ALIGNMENTS

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SOFTWARE: PASTERO
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,588
FILING DATE: 7 June, 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA: 1001uding application PRIOR APPLICATION DATA: 1001uding application PRIOR APPLICATION DATA: 1001uding application PRIOR APPLICATION DATA: 1001uding application PRIOR APPLICATION NUMBER: US/353,784
FILING DATE: 21 october, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 22 october, 1994
APPLICATION NUMBER: U.S. 08/099,389
FILING DATE: 22 Detcher, 1993
APPLICATION NUMBER: U.S. 08/099,389
FILING DATE: 22 PEDICALION; 1001
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                                                                              APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
CORRESPONDENCE: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
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FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
APPLICATION NUMBER: U.S. 07/834,1992
APPLICATION NUMBER: U.S. 07/749,451
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JMBER: U.S. 08/017,127
12 February, 1993
JMBER: U.S. 07/934,161
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MEDIUM TYPE: 3.5" Diskette, 1.44
COMPUTER: IBM PC compatible
OPBRATING SYSTEM: PC-DOS/MS-DOS
Sequence 8, Application US/08485588 Patent No. 5688938
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APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: G13 West Fifth Street
CITY: Los Angeles
STATE: California
                                  NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 31.79
REFERENCE/DOCKET NUMBER: 213/005
TELECOMMUNICATION INPORMATION:
TELEPHONE: (213) 489-1600
TELER: 67-3510
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1079 amino acids
TYPE: amino acids
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Patent No. 5763569
23 August, 1991
FILING DATE: 23 August, 1 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-485-588-8
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                             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                    application below: 9
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
PCT/US/94/1/2117
FILING DATE: 9 December, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/11,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/019,389
FILING DATE: 23 Adgust, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/334,161
FILING DATE: 21 Adgust, 1993
APPLICATION NUMBER: U.S. 07/334,161
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/344,61
FILING DATE: 21 Adgust, 1992
APPLICATION NUMBER: U.S. 07/344,044
FILING DATE: 23 Adgust, 1991
ATTORNEY AGGNT INFORMATION:
                                                                                                                        SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,565
FILING DATE: 7 June, 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Heber, Sheldon O. REGISTRATION NUMBER: 38,179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 21.
TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Di
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295 --NLVPEFRGVMKVDINLQKVDIDQCSSDGWFSGTHKCHLNNS------ECMPIKG 342
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                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                   95;
                                                                                                                                                                 Length 1079;
                                                                                                                                                                                                                   Indels
                                                                                                                                                            4.2%; Score 133.5; DB 2;
21.7%; Pred. No. 0.00056;
tive 58; Mismatches 182;
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COMPUTER READBLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,986
FILING DATE: 03-0CT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/08943986 Patent No. 5962314
  LENGTH: 1079 amino acids
                                                                                                                                                               Query Match 4.2%
Best Local Similarity 21.7%
Matches 93; Conservative
                                         , ALEL GUILLO GCIG
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-480-751-8
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PRIOR APPLICATION DATA:
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STATE: California
                                amino acid
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668 FIGEPQDWTCRLRQPAFGISFVLCISCILVKTNRVLLVFEAKIPTSFHRKWWGLNLQFLL 727
                                                    532 V-----ILLVVFWFLIGWTSSVCQNLEKQISLIGQGKTSDHLIFNMCLIDRWDYMTAV 584
                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Edward F. Nemeth
APPLICANT: Edward F. Nemeth
APPLICANT: Edward M. Brown
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: Steven C. Hebert
APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Suite 4700
STREET: Suite 4700
STREET: G33 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
Including application
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/141,248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER FEADABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: U.S. 08/00/389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 33 August, 1991
ATTONEY AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 313/004
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,751
FILING DATE: 7 June, 1995
CLASSIFICATION: 435
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TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 8:
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774 G--SLIGY 779
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US-08-480-751-8
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4.2%; Score 133.5; DB 2; Length
Best Local Similarity 21.7%; Pred. No. 0.00056;
Matches 93; Conservative 58; Mismatches 182; Indels
               APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: 08/75/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 Aquast, 1994
APPLICATION NUMBER: U.S. 08/11,248
FILING DATE: 23 Aquast, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/001,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 Rebruary, 1992
APPLICATION NUMBER: U.S. 07/934,61
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/934,044
FILING DATE: 23 August, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Heber, Sheldon O. REGISTRATION NUMBER: 38,179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 21.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
7-June-1995
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
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G--SLIGY 779
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CLASSIFICATION: 514
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: 8
APPLICATION NUMBER: PCT/US/94/1217
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/09,389
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4.2%; Score 133.5; DB 3;
Best Local Similarity 21.7%; Pred. No. 0.00056;
Matches 93; Conservative 58; Mismatches 182;
                                                 GENERAL INFORMATION:
APPLICANT: Edward F. Nemeth, Edward M.
APPLICANT: Brown, Steven C. Hebert,
APPLICANT: Brown, Steven C. Hebert,
APPLICANT: Bradford C. Van Wagenen, Manuel
APPLICANT: F. Balandrin, Fortest H. Fuller,
APPLICANT: F. Balandrin, Fortest H. Fuller,
APPLICANT: Eric G. DelNar, and Scott T. Moe
TITLE OF INVENTION: MOLECULES
ITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage COMPUTER: IBM PC compatible comparing
                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
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APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 AUGUST, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 AUGUST, 1991
ATTORNEY AGENT INFORMATION:
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FILING DATE: 9 December, 1994
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; Sequence 8, Application US/08353784; Patent No. 6011068
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 8:
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California
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OPERATING SYSTEM:
SOFTWARE: FASTSEC
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-484-719B-8
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APPLICATION NUMBER:
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                                    -----GAYECICKAG---FYHPGVLPVNNFRRGPDQHIS---- 379
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                                                                                                                                                                   -GSTKDVSEE----AYVCLPCREG------CPFCADD-----SPCFVQEDKYLR 417
                                                                                                                                                                                                                                            ----LAIISFQGLCMLLDFVSMLVVYHFRKAKSIRASGLILLETILFGSLLLYFPVVI 471
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                                                                                                                           NYSIINWHLSPEDGSIVFKEVGYYNVYAKKGERLFINEEKILWSGFSREVPFSNCSRDCQ
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              --NLVPEFRGVMKVDINLQKVDIDQCSSDGWFSGTHKCHLNNS--
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APPLICANT: Edward F. Nemeth, Edward M.
APPLICANT: Brown, Steven C. Hebert,
APPLICANT: Bradford C. Van Wagenen,
APPLICANT: Manuel F. Balandrin,
APPLICANT: Fortest H. Fuller, Eric G.
APPLICANT: Fortest H. Fuller, Eric G.
APPLICANT: Delmar, Scott T. Moe
ITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS WORD
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STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
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CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 08/353,784
APPLICATION NUMBER: 08/353,784
APPLICATION NUMBER: 08/353,784
APPLICATION NUMBER: 08/353,784
APPLICATION NUMBER: 08/353,784
APPLICATION NUMBER: 07/05/94/12117
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APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/09,389
FILING DATE: 23 February, 1993
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APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
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Patent No. 6031003
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STATE: California
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G--SLIGY 779
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377 HEEG---GNRLLNSSTAFRPLCTGDENINSVETPYMDYEHLRISYNVYLAVYSIAHALQD 433
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Patent No. 6313146
GENERAL INFORMATION:
APPLICANT: Bradford C. Van Wagenen
APPLICANT: Manuel F. Balandrin
APPLICANT: Eric G. Del Mar
APPLICANT: Echard F. Nemeth
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
                      FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Douglas C. Murdock
REGISTRATION NUMBER: 37,549
REFERENCE/DOCKET NUMBER: 213/007
TELECOMMUNICATION INFORMATION:
U.S. 08/017,127
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 8:
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LENGTH: 1079 amino acids
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668 FIGEPODWTCRLROPAFGISFVLCISCILVKTNRVLLVFEAKIPTSFHRKWWGLNLOFIL 727
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                                                                                                  -----LAIISFQGLCMLLDFVSMLVVYHFRKAKSIRASGLILLETILFGSLLLYFPVVI 471
                                                                                                                                                              608 WTEPFGIALTLFAVLGIFLTAFVLGVFIKFRNTPIVKATNRELSYLLLFSLLCCFSSSLF 667
                                                                                                                                                                                                                                    LYFEPSTFRCILLRWARLLGFATVYGTVTLKLHRVLKVFLSRTAQRIPYMTGGRVMRMLA 531
                                                                                                                                                                                                                                                                                                                                                                          532 V-----ILLVVFWFLIGWTSSVCQNLEKQISLIGQGKTSDHLIFNMCLIDRWDYMTAV 584
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538 WSGF--SKVVPFSNCSR----DCVPGTRKGIIEGEPTCCFECMACAEGEFSDENDASACT 591
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APPLICANT: H. William Harris
APPLICANT: Hedward M. Brown
APPLICANT: Steven C. Hebert
TITLE OF INVENTION: Polycation-Sensing Receptor in Aquatic
TITLE OF INVENTION: Polycation-Sensing Receptor in Aquatic
TITLE OF INVENTION: Species and Methods of Use Thereof
FILE REFERENCE: 2866.1001-007
CURRENT APPLICATION NUMBER: US/09/162,021B
CURRENT APPLICATION NUMBER: POT/US97
PRIOR FILING DATE: 1998-09-28
PRIOR FILING DATE: 1997-03-27
PRIOR FILING DATE: 1996-03-27
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 1027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.1%; Score 132; DB 4; Length 1027; 19.5%; Pred. No. 0.00073; tive 58; Mismatches 166; Indels 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: squalus acanthias
US-09-162-021B-2
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Matches 88; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GMWSLVSY 592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION DATA:
PRIOR APPLICATION NABER:
PETLING DATE:
POCCODE:
PRIOR APPLICATION NUMBER:
PCT/US/94/12117
FILING DATE:
POCCODE:
PRILING DATE:
PRELICATION NUMBER:
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PRILING DATE:
PRELICATION NUMBER:
PRELICATION POR SEG ID NO:
PREPARAMATION FOR SEG ID NO:
PREPARAMETER PREPARAMETER PREPARAMETER PREPARAMATION:
PROPARAMATION FOR SEG ID NO:
PREPARAMETER PREPARAMETER PREPARAMETER PREPAR
                                                                                                                                                                                                                                                                                                ZIP: 90071

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                        ADDRESSEE: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTX: USA
ZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/484,159
FILING DATE: 7 June, 1995
CLASSIFICATION: 435
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LENGTH: 1079 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FASTSEQ CURRENT APPLICATION DATA:
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                               CORRESPONDENCE ADDRESS:
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| :| :| :| :|:|:588 DFWSNENHTSCIAKEIEFLSWTEPFGIALTLFAVLGIFLTAFVLGVFIKFRNTPIVKATN 647
                                                                                                                                                                        311 QKVDIDQCSSDGWFSGTHKC---HLNNSE-CMPIKGLGFVLGAYECICKAG---FYHPGV 363
                                                                                                                                                                                                                        475 EQVTFDEC---GDLVGNYSIINWHLSPEDGSIVFKEVGY----YNVYAKKGERLFINEEK 527
                                                                                                                                                                                                                                                                                                 405 D-----SPCFVQEDKYLR-----LAIISFQGLCMLLDFVSMLVVYHFRKAKSIRASG 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  452 LILLETILFGSLLLYFPVVILYFEPSTFRCILLRWARLLGFATVYGTVTLKLHRVLKVFL 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                648 RELSYLLEFSLLCCFSSSLFFIGEPQDWTCRLRQPAFGISFVLCISCILVKTNRVLLVFE 707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            708 AKIPTSFHRKWWGLNLQFLLVFLCTFMQIVICVIWLYTAPPSSYRNQELEDEIIFITCHE 767
                                                                                                                                                                                                                                                                     364 LPVNNFRRRGPDQH----ISGSTKDVSEE----AYVCLPCREG-----CPFCAD 404
                                                                                                                             Gaps
                                                                                                                           58;
                                                                           Length 1078;
                                                                        ; Score 127; DB 1; Length 10; Pred. No. 0.0025; 48; Mismatches 139; Indels
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COMPUTER PACKAL
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: 9
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE
TITLE OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Lyon & Lyon
STREET: First interstate World Center
STREET: Suite 4700
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
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APPLICATION NUMBER: PCT/US/94/1611.
FILING DATE: 21 October, 1994
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FILING DATE: 22 October, 1993
APPLICATION NUMBER: 0.5.08/141,248
APPLICATION NUMBER: 0.5.08/009,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,565
FILING DATE: 7 June, 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 7, Application US/08484565
; Patent No. 5763569
                                                                      Query Match
Best Local Similarity 22.5%;
Matches 71; Conservative 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              560 GQGKTSDHLIFNMCLI 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           768 GSLMALGFLIGYTCLL 783
  MOLECULE TYPE: protein
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US-08-485-588-7
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508 KVFLSRTAQRIPYMTGGRVMRMLAVILLV-----VFWFLIGWTSSVCQNLEKQISLIG 560
                                               712 LVFEAKIPTSLHRKWVGLNLQFLLVFLCILVQIVTCIIWLYTAPPSSY-RNHELE---- 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC COMPATIBLE
SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,588
FILING DATE: 7 June, 1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                        Sequence 7, Application US/08485588
Fatent No. 5688938
GENERAL INFORMATION:
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: Forrest H. Fuller:
APPLICANT: Forrest H. Fuller:
APPLICANT: Games E. Garrett, Jr.
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/353,784
APPLICATION NUMBER: PCT/US/94/12117
APPLICATION NUMBER: DCT/US/94/12117
APPLICATION NUMBER: U.S. 08/292,827
APPLICATION NUMBER: U.S. 08/292,827
                                                                                               561 QGKTSDHLIFNMCLIDRWDYMTAVGMWSLVSY 592
                                                                                                                                -----DEVIFITC-----DEGSLMALGFLIGY 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSE: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 470
STREET: 633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
FILING DATE: 22 October, 1993
FILING DATE: 33 Rebruary, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 33 Rebruary, 1993
APPLICATION NUMBER: U.S. 08/017,127
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APPLICATION NUMBER: 0.5.07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38,179
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Los Angeles
STATE: California
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California
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                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          311 QKVDIDQCSSDGWFSGTHKC---HLNNSE-CMPIKGLGFVLGAYECICKAG---FYHPGV 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        364 LPVNNFRRRGPDQH-----ISGSTKDVSEE----AYVCLPCREG------CPFCAD 404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          452 LILLETILFGSLLLYFPVVILYFEPSTFRCILLRWARLLGFATVYGTVTLKLHRVLKVFL 511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          708 AKIPTSFHRKWWGLNLQFLLVFLCTFMQIVICVIWLYTAPPSSYRNQELEDEIIFITCHE 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4.0%; Score 127; DB 1; Length 10<sup>2</sup> 22.5%; Pred. No. 0.0025; tive 48; Mismatches 139; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Edward F. Nemeth
APPLICANT: Edward M. Brown
APPLICANT: Edward M. Brown
APPLICANT: Steven C. Hebert
APPLICANT: James B. Garrett, Jr.
TITLE OF INVENTION: MOLECULES
INUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSE: Lyon & Lyon
STREET: First Interstate World Center
STREET: Suite 4700
STREET: Suite 4700
STREET: Suite 4700
STREET: Los Angeles
               APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
                                                                                                                                                                  ATTORNEY/AGENT INFORMATION: 07.5. 07/743

ATTORNEY/AGENT INFORMATION: NAME: Heber, Sheldon 0. REGISTRATION NUMBER: 31,79

REFERENCE/DOCKET NUMBER: 213/00

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERICS: (213) 489-1600

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERICS: (213) 250-0470

INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERICS: (213) 250-0470

INFORMATION FOR SEQ ID NO: 7: SEQUENCE CHARACTERICS: (213) 250-0470
23 February, 1993
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Matches 71; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
  FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  364 LPVNNFRRRGPDQH-----ISGSTKDVSEE----AYVCLPCREG------CPFCAD 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  528 ILWSGFSREVPFSNCSRDCLAGTRKGIIEGEPTCCFECVECPDGEYSDETDASACNKCPD 587
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        452 LILLETILFGSLLLYFPVVILYFEPSTFRCILLRWARLLGFATVYGTVTLKLHRVLKVFL 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           512 SRTAQRIPYMTGGRVMRMLAV-----ILLVVFWFLIGWTSSV-CONLEKQISLI---- 559
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                                                                                                                                                                      APPLICATION NUMBER: US/08/480,751
FILING DATE: 7 June, 1995
CLASSIECATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: electrication
PRIOR APPLICATION DATA: 10104
FILING DATE: 9 December, 1994
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
                             3.5" Diskette, 1.44 Mb storage
                                                                                                                                                                                                                                                                                                                                   APPLICATION.
FILING DATE: 9 Decem.
FILING DATE: 10 Decem.
APPLICATION NUMBER: PCT/US/>**, APPLICATION NUMBER: 0.5. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: 0.5. 08/141,248
APPLICATION NUMBER: 0.5. 08/141,248
APPLICATION NUMBER: 0.5. 08/09,389
-vc. DATE: 22 October, 1993
-vc. DATE: 22 October, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 August, 1992
APPLICATION NUMBER: U.S. 07/934,61
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
FILING DATE: 33 August, 1991
ATTONNEY,AGGNT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/004
                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTERN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
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LENGTH: 1078 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (213) 955-0440
                                                                                                                                              CURRENT APPLICATION DATA:
COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE: protein US-08-480-751-7
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Length 1078;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                               APPLICANT: Steven C. Hebert
APPLICANT: James E. Garrett, Jr.
TITLE OF INVEWIION: CALCIUM RECEPTOR-ACTIVE
TITLE OF INVENTION: MOLECULES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/484,565
FILING DATE: 7-June-1995
APPLICATION NUMBER: 08/353,784
FILING DATE: 9 December, 1994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 08/011,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 12 Hebruary, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 13 August, 1992
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
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First Interstate World Center
Suite 4700
633 West Fifth Street
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,986
FILING DATE: 03-OCT-1997
CLASSIFCATION: 530
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TELECOMNUMICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFA: (213) 955-0440
TELEFA: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                              Sequence 7, Application US/08943986 Patent No. 5962314 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 23 August, 1991
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                           APPLICANT: Edward M. Brown
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560 GQGKTSDHLIFNMCLI 575
                                           768 GSLMALGFLIGYTCLL 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 530
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Los Angeles
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                            US-08-943-986-7
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Best Local Similarity

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13;
                                                    311 QKVDIDQCSSDGWFSGTHKC---HLNNSE-CMPIKGLGFVLGAYECICKAG---FYHPGV 363
                                                                                                   475 EQVTFDEC---GDLVGNYSIINWHLSPEDGSIVFKEVGY----YNVYAKKGERLFINEEK 527
                                                                                                                                                                                 D-----SPCFVQEDKYLR-----LAIISFQGLCMLLDFVSMLVVYHFRKAKSIRASG 451
                                                                                                                                                                                                                                                                                                  588 DFWSNENHTSCIAKEIEFLSWTEPFGIALTLFAVLGIFLTAFVLGVFIKFRNTPIVKATN 647
                                                                                                                                                                                                                                                                                                                                                      452 LILLETILFGSLLLYFPVVILYFEPSTFRCILLRWARLLGFATVYGTVTLKLHRVLKVFL 511
                                                                                                                                                                                                                                                                                                                                                                                     512 SRTAQRIPYMTGGRVMRMLAV-----ILLVVFWFLIGWTSSV-CQNLEKQISLI---- 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              364 LPVNNFRRRGPDQH-----ISGSTKDVSEE----AYVCLPCREG-------CPFCAD 404
     Gaps
58;
  Mismatches 139; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: Ja.,
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: including application
PRIOR APPLICATION DATA: described below: 8
APPLICATION NUMBER: PCT/US/94/12117
TILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/29, 827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/141, 248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009, 389
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 08/017, 127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 08/017, 127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 08/017, 127
FILING DATE: 12 August, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: BCWard F. Nemeth, Edward M.
APPLICANT: Brown, Steven C. Hebert,
APPLICANT: Brown, Steven C. Hebert,
APPLICANT: Bradford C. Van Wagenen, Manuel
APPLICANT: F. Balandrin, Fortest H. Fuller,
APPLICANT: F. Balandrin, Fortest H. Fuller,
APPLICANT: Eric G. DelMar, and Scott T. Moe
TITLE OF INVENTION: MOLECULES
ITLE OF INVENTION: MOLECULES
INVENTED OF INVENTION: MOLECULES
CORRESPONDENCE: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Lyon & Lyon
First Interstate World Center
Suite 4700
633 West Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/353,784
FILING DATE: 9 December, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/08353784 Patent No. 6011068
  48;
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        560 GQGKTSDHLIFNMCLI 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            768 GSLMALGFLIGYTCLL 783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FASTSEQ CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 9 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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  71;
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STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
US-08-353-784-7
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     Matches
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3.5" Diskette, 1.44 Mb storage
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ATTORNEY/AGENT INFORMATION:
NAME: DOUGLAS C. MUXGOCK
REGISTRATION NUMBER: 37,549
REFERENCE/DOCKET NUMBER: 213/007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
                                                                                                                                              7 June, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            560 GQGKTSDHLIFNMCLI 575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-484-7198-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 71; Conserv
                                                                                                                                                FILING DATE: 7
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        528 ILWSGFSREVPFSNCSRDCLAGTRKGIIEGEPTCCFECVECPDGEYSDETDASACNKCPD 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            452 LILLETILFGSLLLYFPVVILYFEPSTFRCILLRWARLLGFATVYGTVTLKLHRVLKVFL 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             708 AKIPTSFHRKWWGLNLQFLLVFLCTFMQIVICVIWLYTAPPSSYRNQELEDEIIFITCHE 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            648 RELSYLLIFSLICCESSSIFFIGEPQDWTCRLRQPAFGISFVLCISCILVKTNRVLLVFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           512 SRTAQRIPYMTGGRVMRMLAV-----ILLVVFWFLIGWTSSV-CQNLEKQISLI----
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1078;
                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 4.0%; Score 127; DB 3; Length 10 Best Local Similarity 22.5%; Pred. No. 0.0025; Matches 71; Conservative 48; Mismatches 139; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Edward F. Nemeth, Edward M. APPLICANT: Brown, Steven C. Hebert, APPLICANT: Bradford C. Van Wagenen, APPLICANT: Manuel F. Balandrin, APPLICANT: Manuel F. Balandrin, APPLICANT: Delmar, Scott T. Moe TITLE OF INVENTION: CALCIUM RECEPTOR-ACTIVE TITLE OF INVENTION: MOLECULES NUMBER OF SEQUENCES: 20 CORRESPONDENCE ADDRESS:
FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/834,044
FILING DATE: 13 August, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 209/069
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEE: Lyon & Lyon
: First Interstate World Center
: Suite 4700
: 53 West Fifth Street
Los Angeles
California
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                                                                                                                                                                                                       TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARATTERISTICS:
LENGTH: 1078 amino acids
TYPE: amino acid
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-08-353-784-7
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                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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311 QKVDIDQCSSDGWFSGTHKC---HLNNSE-CMPIKGLGFVLGAYECICKAG---FYHPGV 363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          405 D-----SPCFVQEDKYLR-----LAIISFQGLCMLLDFVSMLVVYHFRKAKSIRASG 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               452 LILLETILFGSLLLYFPVVILYFEPSTFRCILLRWARLLGFATVYGTVTLKLHRVLKVFL 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     512 SRTAQRIPYMTGGRVMRMLAV-----ILLVVFWFLIGWTSSV-CQNLEKQISLI---- 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364 LPVNNFRRRGPDQH----ISGSTKDVSEE----AYVCLPCREG-----
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS Word
SOFTWARE: FastSEG for Windows Version 3.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,719B
                                                                                                                                                                                                                            DRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/353,784
APPLICATION NUMBER: 08/353,784
APPLICATION NUMBER: 0994
APPLICATION NUMBER: PCT/US/94/12117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 AUGUST, 1994
APPLICATION NUMBER: U.S. 08/141,248
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/009,389
FILING DATE: 23 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 21 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 21 AUGUST, 1993
APPLICATION NUMBER: U.S. 07/934,044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 11 February, 1992
APPLICATION NUMBER: U.S. 07/749,451
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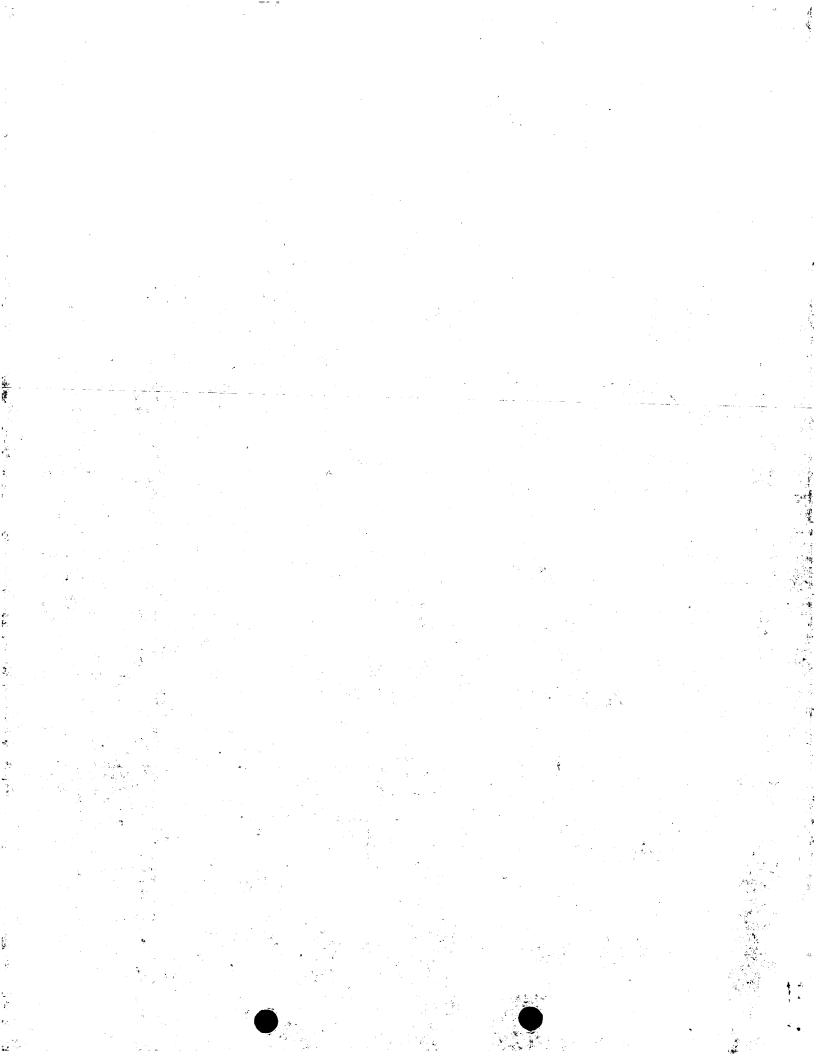
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Query Match 4.0%; Score 127; DB 4; Length 1078; Best Local Similarity 22.5%; Pred. No. 0.0025; Matches 71; Conservative 48; Mismatches 139; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/353,784
APPLICATION NUMBER: 08/353,784
APPLICATION NUMBER: 08/354,72117
FILING DATE: 21 October, 1994
APPLICATION NUMBER: U.S. 08/292,827
FILING DATE: 23 August, 1994
APPLICATION NUMBER: U.S. 08/09,389
FILING DATE: 22 October, 1993
APPLICATION NUMBER: U.S. 08/00,389
FILING DATE: 22 Pebruary, 1993
APPLICATION NUMBER: U.S. 08/017,127
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,161
FILING DATE: 12 February, 1993
APPLICATION NUMBER: U.S. 07/934,61
FILING DATE: 11 February, 1993
APPLICATION NUMBER: U.S. 07/934,61
FILING DATE: 11 FEBRUARY, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
                                                                                               APPLICANT: Bradford C. Van Wagenen
APPLICANT: Manuel F. Balandrin
APPLICANT: Manuel F. Balandrin
APPLICANT: Edward F. Nemeth
TITLE OF INVENTION: MOLECULES
TITLE OF INVENTION: MOLECULES
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: Slirst Interstate World Center
STREET: Slite 4700
STREET: Glite 4700
STREET: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FASTSEQ
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,159
FILING DATE: 7 June, 1995
                            Sequence 7, Application US/08484159 Patent No. 6313146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERNCE/DOCKET NUMBER: 214/
TELECOMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Heber, Sheldon O. REGISTRATION NUMBER: 38,179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1078 amino acids
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                                                                              GENERAL INFORMATION:
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US-08-484-159-7
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311 QKVDIDQCSSDGWFSGTHKC---HLNNSE-CMPIKGLGFVLGAYECICKAG---FYHPGV 363

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528 ILWSGFSREVPFSNCSRDCLAGTRKGIIEGEPTCCFECVECPDGEYSDETDASACNKCPD 587
                                                                                                                                          512 SRTAQRIPYMTGGRVMRMLAV-----ILLVVFWFLIGWTSSV-CQNLEKQISLI---- 559
                                                                                                                                                                                                                                                                                          475 EQVTFDEC---GDLVGNYSIINWHLSPEDGSIVFKEVGY----YNVYAKKGERLFINEEK 527
                                      364 LPVNNFRRGPDQH----ISGSTKDVSEE----AYVCLPCREG------CPFCAD 404
                                                                                                                405 D-----SPCFVQEDKYLR-----LAIISFQGLCMLLDFVSMLVVYHFRKAKSIRASG 451
                                                                                                                                                                                          452 LILLETILFGSLLLYFPVVILYFEPSTFRCILLRWARLLGFATVYGTVTLKLHRVLKVFL 511
                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: February 13, 2003, 02:30:33 Job time: 20.5573 secs
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February 13, 2003, 00:15:14; Search time 8.58545 Seconds (without alignments) 1782.525 Million cell updates/sec
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3199
1 MGAMAYPLLICLLLAQLGLG.......YMTAVGMWSLVSYDGLTIFQ 599
5.1.3
Compugen Ltd.
version
- 2003
                                                                    protein search, using sw model
GenCore
Copyright (c) 1993
                                                                                                                                                                             Title:
Perfect score:
                                                                    OM protein
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Run on:

140259 segs, 25548876 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence: Searched:

al number of hits satisfying chosen parameters: Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries length: 0 length: 2000000000 imum DB seq imum DB seq

/cgn2\_6/ptodata/1/pubpaa/USO8\_NEW\_PUB.pep:\*
/cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep:\*
/cgn2\_6/ptodata/1/pubpaa/USO6\_NEW\_PUB.pep:\*
/cgn2\_6/ptodata/1/pubpaa/USO6\_NEW\_PUB.pep:\*
/cgn2\_6/ptodata/1/pubpaa/USO7\_PUBCOMB.pep:\*
/cgn2\_6/ptodata/1/pubpaa/USO7\_PUBCOMB.pep:\*
/cgn2\_6/ptodata/1/pubpaa/USO7\_PUBCOMB.pep:\*
/cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep:\*
/cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep:\*
/cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep:\*
/cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep:\*
/cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep:\*
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//cgn2\_6/ptodata/1/pubpaa/USO8\_PUBCOMB.pep:\* Published\_Applications\_AA:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Description	Sequence 4, Appli		Sequence 2, Appli	2,	4	5, 4	2, 4	4	800	Sequence 272, App	Sequence 4, Appli	Sequence 6, Appli	Sequence 14, Appl	ď		Sequence 28, Appl	Sequence 2, Appli	Sequence 4, Appli	
ID	US-09-775-181-4	US-09-775-181-2	US-10-002-854-2	US-09-727-205-2	US'-10-027-923-4	US-10-027-923-5	US-09-795-232-2	US-09-816-685-4	US-09-764-853-800	US-09-764-898-272	US-09-799-629-4	US-09-897-427A-6	US-09-796-338A-14	US-09-817-464-2	US-09-737-149-29	US-09-801-196-28	US-09-858-546-2	US-09-819-946-4	US-09-897-427A-2
DB	10	10	12	10	12	12	10	10	10	10	6	σ	10	10	10	10	6	10	6
Query Match Length DB	599	1215	1078	1078	1212	1203	797	828	800	800	850	852	852	912	3313	699	530	763	841
Query Match	100.0	97.5	4.0	3.9	3.6	3.5	3.4	3.4	3.3	3.3	3.2	3.5	3.2	3.5	3.1	3.1	3.1	3.1	3.1
Score	3199	3119.5	127	124	114	111	107.5	107.5	104	104	101.5	101.5	101.5	101	100.5	66	98.5	98.5	98.5
Result No.	∺	7	რ	4	S	9	7	80	σ	10	11	. 12	13	14	15	16	17	18	19

Sequence 17, Appl Sequence 2, Appli Sequence 4, Appli Sequence 12, Appli Sequence 14, Appli Sequence 200, Appli Sequence 5, Appli Sequence 8, Appli Sequence 10, Appli Sequence 10, Appli Sequence 2, Appli Sequence 15, Appli Sequence 16, Appli Sequence 408, Appl	
US-09-799-629-17  US-09-819-946-2  US-10-03-356-8  US-10-09-817-464-12  US-09-817-464-12  US-09-817-464-12  US-09-917-464-12  US-09-918-322-5  US-10-09-454-2  US-09-918-2209  US-10-175-738-408  US-10-175-738-408  US-10-175-738-408  US-10-175-738-408	
84 1148 9915 9915 9915 9916 9916 9916 9916 9916	
99 8 8 8 8 8 8 8 8 8 8 9 8 9 8 9 9 9 9	
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# ALIGNMENTS

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WSRSTDGTILAQKLAEEVPMDVASYLYTGDSHQLKRANCSGRYELAGLPGKWPALASAHP 120
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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          Sequence 4, Application US/09775181

Patent No. US20020038013a1

Patent No. US20020038013a1

APPLICANT: HIDONO, Gregory

APPLICANT: Hilbun, Erin

TITLE OF INVENTION: No. US20020038013Alel Human Membrane Proteins and

TITLE OF INVENTION: Polynucleotides Encoding the Same

FILE REFERENCE: LEX-0129-USA

CURRENT APPLICATION NUMBER: US/09/775,181

CURRENT PILING DATE: 2001-02-01

PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGAMAYPLLLCLLLAQLGLGAVGASRDPQGRPDSPRERTPKGKPHAQQPGRASASDSSAP 60
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100.0%; Pred. No. 1.2e-263;
tive 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-775-181-4
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  Matches 599;
                                                                                                                                                                                                                                                           SEQ ID NO 4
LENGTH: 599
US-09-775-181-4
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APPLICANT: Donobo, Gregory
APPLICANT: Hibbun, Erin
TITLE OF INVENTION: No. US20020038013A1el Human Membrane Proteins and
TITLE OF INVENTION: Polynucleotides Encoding the Same
TITLE OF INVENTION: Polynucleotides Encoding the Same
FILE REFERENCE: LEX-0129-USA
CURRENT APPLICATION NUMBER: US/09/775,181
PRIOR APPLICATION NUMBER: US 60/180,414
PRIOR PILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 5
SOFTWARE: RestSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1215
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                                                                                                    ISFQGLCMLLDFVSMLVVYHFRKAKSIRASGLILLETILFGSLLLYFPVVILYFEPSTFR 480
                                                                                                                                                CILLRWARLLGFATVYGTVTLKLHRVLKVFLSRTAQRIPYMTGGRVMRMLAVILLVVFWF 540
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                                                                                         PGVLPVNNFRRGPDQHISGSTKDVSEEAYVCLPCREGCPFCADDSPCFVQEDKYLRLAI
                                                                                                                                                                                           DSLSAPAPQVFLQATREESRILLQDLSSSAPHLANATLETEWFHGLRRKWRPHLHRRGPN
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QGPRGLGHSWRRKDGLGGDKSHFKWSPPYLECENGSYKPGWLVTLSSAIYGLOPNLVPEF
            RGVMKVDINLQKVDIDQCSSDGWFSGTHKCHLNNSECMPIKGLGFVLGAYECICKAGFYH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09775181 Patent No. US20020038013A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.5%;
98.5%;
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nes 585; Conservative
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RGVMKVDINLOKVDIDOCSSDGWFSGTHKCHLNNSECMPIKGLGFVLGAYECICKAGFYH 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311 QKVDIDQCSSDGWFSGTHKC---HLNNSE-CMPIKGLGFVLGAYECICKAG---FYHPGV 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             364 LPVNNFRRRGPDQH-----ISGSTKDVSEE----AYVCLPCREG-------CPFCAD 404
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                                                                                                                  PGVLPVNNFRRGPDQHISGSTKDVSEEAYVCLPCREGCPFCADDSPCFVQEDKYLRLAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Scadden, David T.
APPLICANT: Scadden, David T.
APPLICANT: Poznansky, Mark C.
APPLICANT: Olszak, Ivona T.
APPLICANT: Brown, Edward M.
TITLE OF INVENTION: THE CAR RECEPTOR AS A MEDIATOR OF
TITLE OF INVENTION: MIGRATORY CELL CHEMOTAXIS AND/OR CHEMOKINESIS
TITLE OF INVENTION: MIGRATORY CELL CHEMOTAXIS AND/OR CHEMOKINESIS
TITLE OF INVENTION NUMBER: US/10/002,854
CURRENT PILING DATE: 2001-11-01
PRIOR FILING DATE: 2000-06-02
                                                                                                                                                                                                                                                                              LIGWISSVCQNLEKQISLIGQGKTSDHLIFNMCLIDRWDYMTAVG-----MWSL 589
                                                                                                                                                                                                                                                                                                                594
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Pred. No. 0.026;
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LOCATION: (1)...(1078)
; OTHER INFORMATION: Ca-sensing Receptor
US-10-002-854-2
                                                                                                                                                                                                                                                                                                                                                                                              US-10-002-854-2; Sequence 2, Application US/10002854; Patent No. US/20020132224A1; GENERAL INFORMATION:
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312 KVDIDQCSSDGWFSGTHKCHLNNSECMPIKGLGFVLGAYECICKAGFYHPGVLPV---- 366
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Patent No. US20020142330A1
GENERAL INFORMATION:
                                                                                                                                                                          Conservative
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   ORGANISM: Homo sapiens
                                                                                                       Query Match
Best Local Similarity
Matches 80; Conserv
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                     ; ORGANISM: H
US-10-027-923-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       648 RELSYLLIFSLLCCFSSSLFFIGEPQDWTCRLRQPAFGISFVLCISCILVKTNRVLLVFE 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311 QKVDIDQCSSDGWFSGTHKC---HLNNSE-CMPIKGLGFVLGAYECICKAG---FYHPGV 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D-----SPCFVQEDKYLR-----LAIISFQGLCMLLDFVSMLVVYHFRKAKSIRASG 451
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Patent No. US20020142330A1
GENERAL INFORMATION:
APPLICANT: Briann Gaither Bates
APPLICANT: Kamalaka Gulukota
APPLICANT: Yuhong Xie
APPLICANT: Janet Elizabeth Paulsen
TITLE OF INVENTION: NOVEL GLUTAMATE RECEPTOR MODULATORY PROTEINS AND
TITLE OF INVENTION: NOVEL GLUTAMATE RECEPTOR MODULATORY PROTEINS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | : | : | | : | : | : | DFWSNENHTSCIAKEIEFLSWTEPFGIALTLFAVLGIFLTAFVLGVFIKFRNTPIVKATN
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                                                                                                                                                        Sequence 2, Application US/09727205
Patent No. US20020064813A1
GENERAL INFORMATION:
APPLICANT: ELLIS. CATHERINE E.
TITLE OF INVENTION: MONKEY CALCIUM SENSING RECEPTOR
FILE REFERENCE: GP-70665
CURRENT APPLICATION UNMBRR: US/09/727,205
CURRENT FILING DATE: 2000-11-30
PRIOR PILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FASTERQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               364 LPVNNFRRRGPDQH----ISGSTKDVSEE----AYVCLPCREG----
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CURRENT APPLICATION NUMBER: US/10/027,923
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/257,589
PRIOR FILING DATE: 2000-12-22
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: MACACA CYNOMOLGUS
109-727-205-2
768 GSLMALGFLIGYTCLL 783
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LENGTH: 1078
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                                                                                                                                                                                                                                                                                        403 -----ADD-SPCFVQEDKYLR-----LAIISFQGLCMLLDFVSMLVVYHFRKAKSIRA 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  613 SSRELCYIILAGICLGYLCTFCLIAKPKQIYCYLQRIGIGLSPAMSYSALVTKTNRIARI 672
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                                                                                                                               219 ETEWFHGLRRKWRPHLHRRGPNQGPRGLGHSWR----RKDGLGGDKSHFKWSPPYLECE 273
                                                                                                                                                                                                                                                      274 NG-----SYKPGWLV-TLSSAIYGL---QPNLVPEFRGV-------MKVDINLQ 311
                                                                                                                                                                                                                                                                                                                                                                      312 KVDIDQCSSDGWFSGTHKCHLNNSECMPIKGLGFVLGAYECICKAGFYHPGVLPVNNFRR 371
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                                                                          Gaps
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APPLICANT: Kamalaka Gulukota
APPLICANT: Kamalaka Gulukota
APPLICANT: Tubnog Xia.
TUTLE OF INVENTION: NUCLEIC ACID MOLECULES AND USES THEREFOR
TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND USES THEREFOR
FILE REFERENCE: GNN 024
CURRENT APPLICATION NUMBER: US/10/027,923
CURRENT FILING DATE: 2001-12-21
PRIOR FILING DATE: 2000-12-22
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               Length 1212;
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Query Match 3.5%; Score 111; DB 12; Best Local Similarity 20.8%; Pred. No. 0.69; Matches 80; Conservative 54; Mismatches 171;
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261 SVWKAIPALQGCGIAMLIISVLIAIY-YNVIICYTLFYLFASFVSVLPWGSCNNPWNTPE 319
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                                                                                       US-09-764-853-800
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US-09-816-685-4
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Best Local S
Matches 61
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| : | | : | | : | 1 STANFIGUS PGRYELANFKEMG---KDYFDYINVGSWDNGELKMDDDEV 498
                                                                                                       DDLTGCDLIPVQYLRWGDPEPIAAVVFACLGLLATLFVTVIFIIYRDTPVVKSSSRELCY 618
                                   ----CPFC----A 403
                                                                                DD-SPCFVQEDKYLR-----LAIISFQGLCMLLDFVSMLVVYHFRKAKSIRASGLILLE 456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 NKSREQNLQDDLDWYQALVWSLLEGEPSISRAAITFSTDSLSAPAP-QVFLQATREESRI 201
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                                                  TILFGSLLLYFPVVILYFEPSTFRCILLRWARLLGFATVYGTVTLKLHRVLKVFLSRTAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138 KGTLERNNTPVVGWV------NMSOSTVVLGTDGITSVLPGSVATVATQED---
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                                   ----NNFRRRGPDQHI-SGSTKDVSEE----AYVCLPCREG--
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                                                                                                                                                                                                                                                            Sequence 2, Application US/09795232 Patent No. US20010012627A1
                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Anthony M. Brown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sest Local Similarity 20.2 Matches 113; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-795-232-2
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US-09-795-232-2
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APPLICANT: CHANDRAMOULISWARAN, ISHWAR et al
TITLE OF INVENTION: ISOLAFED HUMAN G-PROTEIN COUPLED
TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
TITLE OF INVENTION: PROTEINS, AND USES THEREOF
FILE REFERENCE: CLO000856
CURRENT APPLICATION NUMBER: US/09/816,685
CURRENT FILING DATE: 2001-03-26
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                       ----KYFVLKISAGIEYPGEIRWPLALCL 400
                                                                                                                                                                                                                                                           328 HK------CHLNNSECMPIKGLGFVLGAYECICKAGFYHPGVLPVNNFRRRGPDQHI 378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E-----NVLSKCSDSCQPGEY-----KKTAEGQHTC-----CYECLAC 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          396 REG-----CPFC----ADDSPCFVQEDKYLR-----LAIISFQGLCMLLD 431
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                                                                                                            SGSTKDVSEEAYVCLPCREGCPFCADDSPCFVQEDKYLRLAI ---ISFQG-----LCM
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Patent No. US28020090672A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P1206
CURRENT APPLICATION NUMBER: US/09/764,853
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Pred. No. 0.8;
5; Mismatches
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Similarity 23.5%;
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PYLECEN--GSYKPGWLVTLSSAIYGLQPNLVPEFRGVMKVDINLQKVDIDQCSSDGWFS 325
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                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09799629 Publication No. US20030008344A1 GENERAL INFORMATION:
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Best Local Similarity 20.8%;
Matches 60; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ADLER, JON ELLIOT
APPLICANT: ZOZULYA, SERGEY
APPLICANT: LI, XADONG
APPLICANT: O'CONNELL, SHAWN
APPLICANT: STASZEWSKI, LENA
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SOFTWARE: PatentIn Ver. 2.1
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; ORGANISM: Homo sapiens
US-09-799-629-4
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                                                                                                                                                                                                                                                                                                                                .; LOCATION: (687)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-853-800
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   685 NEXEQVPKPCAHQCSNTPGSFKCICPPGQHLLGDGKSCAGLERLPNYGTQYSSYNLARFS 744
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 939
SEQ ID NO 800
LENGTH: 800
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23.5%; Pred. No. 1.5;
live 20; Mismatches 74; Indels 4
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APPLICANT: Rosen et al.
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REPERENCE: P2721
CURRENT PELLING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 311
SOFTWARR: Patentin Ver. 2.0
LENGTH: 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 23.5
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Matches 43; Conservative
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NAME/KEY: SITE
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LOCATION: (197
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609 PDQHCKNTRGGYK-----CIDLCPN-----GMTKAE-NGTCIDIDECK----D 646
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                                                                                 GTHKCHLNNSECMPIKGLGFVLGAYECICKAGFYHPGVLPVNNFRRGPDQHISGSTKDV.385
                                                                                                                                                                                                                                                           291 GLQPNL--VPEFRGVMKVDINLQKVDIDQCSSDGWFSGTHKCHLNNSECMPIKGLGFVLG 348
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CURRENT FILING DATE: 2001-03-07

PRIOR APPLICATION NUMBER: 60/187,546

PRIOR PILING DATE: 2000-04-07

PRIOR APPLICATION NUMBER: 60/195,536

PRIOR FILING DATE: 2000-04-07

PRIOR FILING DATE: 2000-06-06

PRIOR FILING DATE: 2000-06-23

PRIOR FILING DATE: 2000-06-23

PRIOR FILING DATE: 2000-06-23

PRIOR FILING DATE: 2000-06-17

PRIOR FILING DATE: 2000-08-17

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PRIOR FILING DATE: 2000-08-17
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; Pred. No. 2.7;
47; Mismatches 107;
                                                                                                                                              647 GTHOCRYNOI-CENTR----GSYRCVCPRGYRSOGV---
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Page

16;

Gaps

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GENERAL INFORMATION:
APPLICANT: Flor, Peter J.
APPLICANT: Kuhn, Ranier
APPLICANT: Minh, Ranier
APPLICANT: Minh, Ranier
APPLICANT: Lindaur, Kristen
APPLICANT: Lindaur, Kristen
APPLICANT: Indaur, Kristen
APPLICANT: Indaur, Kristen
APPLICANT: Independent of the compounds
TITLE OF INVENTION: Human Metabotropic Glutamate Receptor Subtypes (HMR4, TITLE OF INVENTION: HMR6, HMR7) and Related DNA Compounds
TITLE OF INVENTION: HMR6, HMR7) and Related DNA Compounds
TITLE OF INVENTION: HMR6, HMR7) and Related DNA Compounds
TITLE OF INVENTION: HMR6, HMR7) and Related DNA Compounds
CURRENT FILING DATE: 1996-03-16
EARLIER FILING DATE: 1994-08-19
EARLIER FILING DATE: 1994-08-19
EARLIER FILING DATE: 1994-08-19
EARLIER FILING DATE: 1993-09-20
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
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SEQ ID NO 2
SEQ ID NO 2
SED ID NO 3
SED ID NO 
                                                                                                                                                                                                                                                                                                                                                                                           291 GLQPNL--VPEFRGVMKVDINLQKVDIDQCSSDGWFSGTHKCHLNNSECMPIKGLGFVLG 348
                                                                                                                                                                                                                         349 AYECI-CKAGFYHPGVLPVNNFRRGPDQHISGSTKDVSEEAYVCLPCREGCPFCADD-- 405
                                                                                                                                                                                                                                                                                     518 CYDCVDCEAGSY------RQNPD-----DIA-----CTFCGQDEW 546
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                                                                                                                                                           463 GSVPRLHDVGRFNGSLRT----ERLKIRWHTSDNQ-KPVSRCSRQCQEGQVRRVKGFHSC 517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09817464 Patent No. US20020127638A1
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APPLICANT: Milennium Pharmaceuticals, Inc.
TITLE OF INVENTION: 1983, 52881, 2398, 45449, 50289, AND
TITLE OF INVENTION: 1983, 52881, 2398, 45449, 50289, AND
TITLE OF INVENTION: 52872, NOVEL G PROTEIN-COUPLED RECEPTORS AND USES THEREFOR FILE REFERENCE: 10448-020001
CURRENT APPLICATION NUMBER: US/09/796,338A
CURRENT FILING DATE: 2001-02-28
PRIOR FILING DATE: 2000-02-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16;
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                                                                                                                                                    Sequence 6, Application US/09897427A;
Sequence 6, Application US/09897427A;
Patent No. US20020160424A1;
GENERAL INFORMATION:
APPLICANT: ALDLER, JON ELLIOT
APPLICANT: LI, XIADONG
APPLICANT: STAZEWSKI, LENA
APPLICANT: STAZEWSKI, LENA
APPLICANT: EHEVERRI, FERNANDO
TITLE OF INVENTION: TIR HETERO-OLIGOMERIC TASTE RECEPTORS;
FILE REFERENCE: 078003-028258
CURRENT PILLING DATE: 2001-07-03
NUMBER OF SEQ ID NOS: 10
SOCTHARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 852
513 RTAQRIPYMIGGRVMRML-----AVILLVVF-----WFLIGWISSV 548
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14
LENCTH: 852
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ORGANISM: Homo sapiens
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US-09-796-338A-14
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US-09-796-338A-14
                                                                                                                                                       US-09-897-427A-6
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1358 SL-----LDVLPFDDNVCLREPCENYMKCVSVLRFDSSAPFLASASTLFRP-----IQ 1405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 DVASYLY----TGDSHQLKRAN-CSGRYELA-GLPGKWPALASAHPSLHRALDTLTHATN 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135 FLNVMLQSNKSREQNLQDDLD--WYQ----ALVWSLLEGEPSISRAAITFSTDSLSAPAP 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       189 QVFLQATREES----RILLQDLSSSAPHLANATLETEWFHGLRRKWRPHLHRRGPNQGPR 244
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                                                    GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Spaderna, Steven K
APPLICANT: Spinkets, Richard A.
APPLICANT: Spinkets, Richard A.
APPLICANT: Spinkets, Richard A.
APPLICANT: Spinkets, Richard A.
APPLICANT: Spytek, Kimberly A.
TITLE OF INVENTION: Polypeptides and Nucleic Acids Encoding Same FILE REFERENCE: 1596-620 CIP
CURRENT APPLICATION NUMBER: US/09/737,149
CURRENT APPLICATION NUMBER: 60/170,564
PRIOR APPLICATION NUMBER: 60/170,564
PRIOR APPLICATION NUMBER: 60/173,165
PRIOR APPLICATION NUMBER: 60/173,165
PRIOR APPLICATION NUMBER: 60/173,362
PRIOR FILING DATE: 1999-12-27
FRIOR APPLICATION NUMBER: 60/174,404
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 60/174,404
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 60/174,404
PRIOR APPLICATION NUMBER: 60/174,404
PRIOR FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: 60/174,404
PRIOR APPLICATION NUMBER: 60/174,404
PRIOR FILING DATE: 2000-01-07
PRIOR FILING DATE: 2000-01-07
PRIOR FILING DATE: 2000-08-09
NUMBER OF SEQ ID NOS: 49
SOFTWARKE: PATENTIN Ver. 2.0
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                          Sequence 29, Application US/09737149 Patent No. US20020077466A1
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; ORGANISM: Rattus norvegicus
US-09-737-149-29
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LENGTH: 3313
US-09-737-149-29
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